



2618-17-C4-PUS-2.txt
SEQUENCE LISTING

The following Sequence Listing is submitted pursuant to 37 CFR 1.821. A copy in computer readable form is also submitted herewith.

Applicants assert pursuant to 37 CFR 1.821(f) that the content of the paper and computer readable copies of SEQ ID NO:1 through SEQ ID NO:88 submitted herewith are the same.

(1) GENERAL INFORMATION:

- (i) APPLICANT: Frank, Glenn R.
Wu Hunter, Shirley
Wallenfels, Lynda
- (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
- (iii) NUMBER OF SEQUENCES: 88
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SHERIDAN ROSS P.C.
 - (B) STREET: 1700 LINCOLN ST., SUITE 3500
 - (C) CITY: DENVER
 - (D) STATE: CO
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Connell, Gary J.
 - (B) REGISTRATION NUMBER: 32,020
 - (C) REFERENCE/DOCKET NUMBER: 2618-17-C4
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 303/863-9700
 - (B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr
1           5           10           15
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr
          20           25
```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: Xaa = Tyr or Asp
 (B) LOCATION: 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
1           5           10
```

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
1           5           10           15
Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
          20           25
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 8

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
1           5           10           15

Arg Val Leu Asp Pro Ser Lys
                20

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys
1           5           10           15

Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu
                20           25

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp
 1 5 10 15

Glu Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Phe Asn Asp Gln Ile Lys Ser Val Met Glu Pro Xaa Val Phe Lys
 1 5 10 15

Tyr Pro Xaa Ala Xaa Leu
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGRTTTCWA TRAARTCTTC

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTTACATT AAATTTTCA AATTCGATAT

60

| | | | | | | |
|----------------------|------------|------------|------------|------------|------------|-----|
| 2618-17-C4-PUS-2.txt | | | | | | |
| GAAATTTT | CTGGCAATT | GCGTGT | TGTATT | AATCAAGTAT | CTATGTCAAA | 120 |
| AATGGTCACT | GAAAAGTGTA | AGTCAGGTGG | AAATAATCCA | AGTACAGAAG | AGGTGTCAAT | 180 |
| ACCATCTGGG | AAGCTTACTA | TTGAAGATTT | TTGTATTGGA | AATCA | | 225 |

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 565 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) NAME/KEY: CDS
(B) LOCATION: 45..314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

56

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTG | GCA | ATT | TGC | GTG | TTG | TGT | GTT | TTA | TTA | AAT | CAA | GTA | TCT | ATG | TCA | 104 |
| Leu | Ala | Ile | Cys | Val | Leu | Cys | Val | Leu | Leu | Asn | Gln | Val | Ser | Met | Ser | |
| 5 | | | | | 10 | | | | | 15 | | | | | 20 | |
| | | | | | | | | | | | | | | | | |
| AAA | ATG | GTC | ACT | GAA | AAG | TGT | AAG | TCA | GGT | GGA | AAT | AAT | CCA | AGT | ACA | 152 |
| Lys | Met | Val | Thr | Glu | Lys | Cys | Lys | Ser | Gly | Gly | Asn | Asn | Pro | Ser | Thr | |
| | | | | 25 | | | | | 30 | | | | | 35 | | |

2618-17-C4-PUS-2.txt

| | |
|--|-----|
| GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys 40 45 50 | 200 |
| ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly 55 60 65 | 248 |
| TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn Gln 70 75 80 | 296 |
| AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG Lys His Cys Tyr Cys Glu 85 90 | 344 |
| ATATAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC | 404 |
| CTAACATGTT TTGCCTCCAA TTTATTTTAA CAGCAAATTG CTGGAACCTTA CCGTACCGTA | 464 |
| ACTAAATGTT CAAGAAATAC TGAATGTTTA CAAATAGATT ATTATAAATA TTGTAACATT | 524 |
| GTCTAATATT TATAAGAATT ATATAAACTG AATTGCAAAA A | 565 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| |
|--|
| Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln 1 5 10 15 |
| Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn 20 25 30 |
| Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 35 40 45 |
| Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 50 55 60 |
| Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr 65 70 75 80 |
| Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 85 90 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

2618-17-C4-PUS-2.txt

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|---|-----|
| ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA | 48 |
| Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln | |
| 1 5 10 15 | |
| GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT | 96 |
| Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn | |
| 20 25 30 | |
| AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT | 144 |
| Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile | |
| 35 40 45 | |
| GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA | 192 |
| Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys | |
| 50 55 60 | |
| AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA | 240 |
| Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr | |
| 65 70 75 80 | |
| CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA | 270 |
| Arg Pro Asn Gln Lys His Cys Tyr Cys Glu | |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | |
|---|--|
| Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln | |
| 1 5 10 15 | |
| Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn | |
| 20 25 30 | |
| Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile | |
| 35 40 45 | |

2618-17-C4-PUS-2.txt

Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
 50 55 60
 Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
 65 70 75 80
 Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
 85 90

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTGGATCCG TCAAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGAATTCG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 97..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|--|-----|
| CCGAAATCTC CTATCACAGT GTACGGAGTG TAAATATTG TTGAAGTATT TTGAAATTTA | 60 |
| TTAATTTTATT CGAAAAGGAG ATTTTCATTAA ATAAAA ATG GTT TAC GAA AGT GAC | 114 |
| Met Val Tyr Glu Ser Asp | |
| 1 5 | |
| TTT TAC ACG ACC CGT CGG CCC TAC AGT CGT CCG GCT TTG TCT TCA TAC | 162 |
| Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg Pro Ala Leu Ser Ser Tyr | |
| 10 15 20 | |
| TCC GTA ACG GCA CGT CCA GAG CCG GTT CCT TGG GAC AAA TTG CCG TTC | 210 |
| Ser Val Thr Ala Arg Pro Glu Pro Val Pro Trp Asp Lys Leu Pro Phe | |
| 25 30 35 | |
| GTC CCC CGT CCA AGT TTG GTA GCA GAT CCC ATA ACA GCA TTT TGC AAG | 258 |
| Val Pro Arg Pro Ser Leu Val Ala Asp Pro Ile Thr Ala Phe Cys Lys | |
| 40 45 50 | |
| CGA AAA CCT CGC CGA GAA GAA GTT GTT CAA AAA GAG TCC ATT GTT CGA | 306 |
| Arg Lys Pro Arg Arg Glu Glu Val Val Gln Lys Glu Ser Ile Val Arg | |
| 55 60 65 70 | |
| AGG ATC AAT TCT GCA GGA ATT AAA CCC AGC CAG AGA GTT TTA TCG GCT | 354 |
| Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser Gln Arg Val Leu Ser Ala | |
| 75 80 85 | |
| CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT | 402 |
| Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val | |
| 90 95 100 | |
| TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT | 450 |
| Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile | |
| 105 110 115 | |
| TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT | 498 |
| Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg | |
| 120 125 130 | |
| CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG | 546 |
| Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu | |
| 135 140 145 150 | |
| ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG | 598 |
| Thr Thr Phe His Arg Arg Tyr | |
| 155 | |
| AAGTCATGTG GTGTTTTTTTA TACATTCTTT ATTAATCGAT ATTCCTAACG AACGATACGA | 658 |
| TAACTTTTCGA TAACTTTTTC TGGTTAATTT TGACAAAATA TGCATTTGCA AGCATAACAT | 718 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCATTTTCAA | GGCAAACGCT | TTCTGATGAT | TATCTTGTTA | AAAGTGTGGA | AACAAGCGTA | 778 |
| GTGTTAACAA | ATGCATTGCT | TGTTTTGATT | ATTTATTTAT | CTATTATATA | TTCCATATTG | 838 |
| TATTGTAGGT | GGTGTACTTG | GTATTACTAA | TACACGTACT | TTGTGAAAAA | AAAAAAAAAA | 897 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Tyr | Glu | Ser | Asp | Phe | Tyr | Thr | Thr | Arg | Arg | Pro | Tyr | Ser | Arg | 1 | 5 | 10 | 15 |
| Pro | Ala | Leu | Ser | Ser | Tyr | Ser | Val | Thr | Ala | Arg | Pro | Glu | Pro | Val | Pro | 20 | 25 | 30 | |
| Trp | Asp | Lys | Leu | Pro | Phe | Val | Pro | Arg | Pro | Ser | Leu | Val | Ala | Asp | Pro | 35 | 40 | 45 | |
| Ile | Thr | Ala | Phe | Cys | Lys | Arg | Lys | Pro | Arg | Arg | Glu | Glu | Val | Val | Gln | 50 | 55 | 60 | |
| Lys | Glu | Ser | Ile | Val | Arg | Arg | Ile | Asn | Ser | Ala | Gly | Ile | Lys | Pro | Ser | 65 | 70 | 75 | 80 |
| Gln | Arg | Val | Leu | Ser | Ala | Pro | Ile | Arg | Glu | Tyr | Glu | Ser | Pro | Arg | Asp | 85 | 90 | 95 | |
| Gln | Thr | Arg | Arg | Lys | Val | Leu | Glu | Ser | Val | Arg | Arg | Gln | Glu | Ala | Phe | 100 | 105 | 110 | |
| Leu | Asn | Gln | Gly | Gly | Ile | Cys | Pro | Leu | Thr | Thr | Arg | Asn | Asp | Asp | Met | 115 | 120 | 125 | |
| Asp | Arg | Leu | Leu | Pro | Arg | Leu | His | Ser | Ser | His | Thr | Thr | Pro | Ser | Ala | 130 | 135 | 140 | |
| Asp | Arg | Lys | Val | Leu | Leu | Thr | Thr | Phe | His | Arg | Arg | Tyr | 145 | 150 | 155 | | | | |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

ATGGTTTACG AAAGTGACTT TTACACGACC CGTCGGCCCT ACAGTCGTCC GGCTTTGTCT      60
TCATACTCCG TAACGGCACG TCCAGAGCCG GTTCCTTGGG ACAAATTGCC GTTCGTCCCC      120
CGTCCAAGTT TGGTAGCAGA TCCCATAACA GCATTTTGCA AGCGAAAACC TCGCCGAGAA      180
GAAGTTGTTC AAAAAGAGTC CATTGTTCGA AGGATCAATT CTGCAGGAAT TAAACCCAGC      240
CAGAGAGTTT TATCGGCTCC AATAAGAGAA TACGAATCCC CAAGGGACCA GACCAGGCGT      300
AAAGTTTTGG AAAGCGTCAG AAGACAAGAA GCTTTTCTGA ACCAAGGAGG AATTTGTCCA      360
TTGACCACCA GAAATGATGA CATGGATAGA CTTCTACCCC GTCTCCACAG TTCACACACA      420
ACACCTTCTG CGGATAGGAA AGTTTTGTTG ACCACTTTTC ACAGAAGATA C              471

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..2706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GCGG ATG AAG AGC ATC GAG GCT TAT ACA AAC AGA TAT GAA ATC ATA GCT      49
  Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala
    1             5             10             15

TCT GAA ATA GTT AAT CTT CGA ATG AAA CCA GAT GAT TTT AAT TTA ATA      97
Ser Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile
    20             25             30

AAA GTT ATT GGT CGA GGA GCA TTT GGT GAA GTA CAG TTA GTG CGA CAC      145
Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His
    35             40             45

AAA TCA ACT GCA CAA GTT TTT GCT ATG AAA CGC CTA TCA AAA TTT GAA      193
Lys Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu
    50             55             60

ATG ATT AAG AGA CCA GAC TCT GCA TTT TTT TGG GAA GAA CGT CAT ATA      241
Met Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile
    65             70             75

ATG GCT CAT GCA AAA TCA GAA TGG ATT GTA CAA TTA CAT TTT GCT TTT      289

```

2618-17-C4-PUS-2.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | His | Ala | Lys | Ser | Glu | Trp | Ile | Val | Gln | Leu | His | Phe | Ala | Phe | | |
| 80 | | | | | 85 | | | | | 90 | | | | | 95 | | |
| CAA | GAT | CAA | AAA | TAT | CTT | TAT | ATG | GTC | ATG | GAT | TAT | ATG | CCG | GGG | GGT | 337 | |
| Gln | Asp | Gln | Lys | Tyr | Leu | Tyr | Met | Val | Met | Asp | Tyr | Met | Pro | Gly | Gly | | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| GAC | TTG | GTG | AGT | CTT | ATG | TCC | GAT | TAT | GAA | ATT | CCA | GAA | AAA | TGG | GCA | 385 | |
| Asp | Leu | Val | Ser | Leu | Met | Ser | Asp | Tyr | Glu | Ile | Pro | Glu | Lys | Trp | Ala | | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| ATG | TTC | TAT | ACA | ATG | GAA | GTG | GTG | CTA | GCA | CTT | GAT | ACA | ATT | CAC | TCC | 433 | |
| Met | Phe | Tyr | Thr | Met | Glu | Val | Val | Leu | Ala | Leu | Asp | Thr | Ile | His | Ser | | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| ATG | GGA | TTT | GTA | CAT | CGT | GAT | GTT | AAA | CCT | GAT | AAT | ATG | CTT | CTA | GAC | 481 | |
| Met | Gly | Phe | Val | His | Arg | Asp | Val | Lys | Pro | Asp | Asn | Met | Leu | Leu | Asp | | |
| | 145 | | | | | 150 | | | | | 155 | | | | | | |
| AAA | TAT | GGT | CAT | TTA | AAG | TTA | GCT | GAC | TTT | GGA | ACC | TGT | ATG | AAA | ATG | 529 | |
| Lys | Tyr | Gly | His | Leu | Lys | Leu | Ala | Asp | Phe | Gly | Thr | Cys | Met | Lys | Met | | |
| 160 | | | | | 165 | | | | | 170 | | | | | 175 | | |
| GAT | ACA | GAT | GGT | TTG | GTA | CGT | TCT | AAT | AAT | GCT | GTT | GGA | ACG | CCT | GAT | 577 | |
| Asp | Thr | Asp | Gly | Leu | Val | Arg | Ser | Asn | Asn | Ala | Val | Gly | Thr | Pro | Asp | | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| TAC | ATT | TCT | CCC | GAA | GTT | TTG | CAG | TCC | CAA | GGT | GGT | GAA | GGA | GTT | TAC | 625 | |
| Tyr | Ile | Ser | Pro | Glu | Val | Leu | Gln | Ser | Gln | Gly | Gly | Glu | Gly | Val | Tyr | | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| GGT | CGT | GAA | TGC | GAT | TGG | TGG | TCT | GTG | GGA | ATT | TTT | TTG | TAT | GAA | ATG | 673 | |
| Gly | Arg | Glu | Cys | Asp | Trp | Trp | Ser | Val | Gly | Ile | Phe | Leu | Tyr | Glu | Met | | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| TTA | TTT | GGA | GAA | ACA | CCT | TTT | TAT | GCA | GAC | AGT | TTG | GTT | GGA | ACT | TAC | 721 | |
| Leu | Phe | Gly | Glu | Thr | Pro | Phe | Tyr | Ala | Asp | Ser | Leu | Val | Gly | Thr | Tyr | | |
| | 225 | | | | | 230 | | | | | 235 | | | | | | |
| AGT | AAA | ATT | ATG | GAT | CAC | AGA | AAC | TCA | TTA | ACT | TTT | CCT | CCA | GAA | GTG | 769 | |
| Ser | Lys | Ile | Met | Asp | His | Arg | Asn | Ser | Leu | Thr | Phe | Pro | Pro | Glu | Val | | |
| 240 | | | | | 245 | | | | | 250 | | | | | 255 | | |
| GAA | ATA | AGC | CAA | TAT | GCC | CGA | TCT | TTG | ATA | CAA | GGA | TTT | TTA | ACA | GAC | 817 | |
| Glu | Ile | Ser | Gln | Tyr | Ala | Arg | Ser | Leu | Ile | Gln | Gly | Phe | Leu | Thr | Asp | | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| AGA | ACA | CAG | CGT | TTA | GGC | AGA | AAT | GAA | GTG | GAA | GAA | ATT | AAA | CGA | CAT | 865 | |
| Arg | Thr | Gln | Arg | Leu | Gly | Arg | Asn | Glu | Val | Glu | Glu | Ile | Lys | Arg | His | | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| CCA | TTT | TTC | ATA | AAT | GAT | CAA | TGG | ACT | TTT | GAC | AAT | TTA | AGA | GAC | TCT | 913 | |
| Pro | Phe | Phe | Ile | Asn | Asp | Gln | Trp | Thr | Phe | Asp | Asn | Leu | Arg | Asp | Ser | | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| GCC | CCA | CCT | GTA | GTG | CCA | GAG | CTG | AGT | GGT | GAT | GAT | GAT | ACA | AGG | AAC | 961 | |
| Ala | Pro | Pro | Val | Val | Pro | Glu | Leu | Ser | Gly | Asp | Asp | Asp | Thr | Arg | Asn | | |
| | 305 | | | | | 310 | | | | | 315 | | | | | | |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| TTT GAT GAT ATT GAA CGT GAT GAA ACA CCT GAA GAG AAT TTT CCT ATA | 1009 |
| Phe Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile | |
| 320 325 330 335 | |
| CCA AAA ACT TTT GCT GGT AAT CAT CTG CCA TTT GTT GGA TTC ACA TAT | 1057 |
| Pro Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr | |
| 340 345 350 | |
| AAT GGT GAT TAC CAA TTA TTA ACA AAT GGA GGT GTT AGA AAT AGT GAT | 1105 |
| Asn Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp | |
| 355 360 365 | |
| ATG GTT GAT ACA AAA TTA AAC AAC ATT TGT GTT TCA AGT AAG GAT GAT | 1153 |
| Met Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp | |
| 370 375 380 | |
| GTG TTA AAT TTA CAA AAT TTA TTA GAA CAA GAG AAA GGT AAC AGT GAA | 1201 |
| Val Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu | |
| 385 390 395 | |
| AAT TTG AAA ACA AAC ACC CAA TTA TTA AGT AAT AAA TTA GAT GAA CTA | 1249 |
| Asn Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu | |
| 400 405 410 415 | |
| GGT CAG AGA GAA TGT GAA TTA AGG AAT CAG GCT GGA GAT TAT GAG AAA | 1297 |
| Gly Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys | |
| 420 425 430 | |
| GAA TTG ACT AAA TTC AAA TTA TCG TGC AAA GAA TTA CAA CGT AAG GCA | 1345 |
| Glu Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala | |
| 435 440 445 | |
| GAA TTT GAG AAT GAA TTA CGG CGT AAA ACT GAG TCC TTA CTA GTT GAA | 1393 |
| Glu Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu | |
| 450 455 460 | |
| ACA AAG AAA AGA CTA GAC GAA GAG CAG AAT AAA AGA ACT AGA GAA ATG | 1441 |
| Thr Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met | |
| 465 470 475 | |
| AAT AAT AAT CAA CAG CAC AAT GAC AAA ATA AAT ATG TTA GAA AAA CAA | 1489 |
| Asn Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln | |
| 480 485 490 495 | |
| ATT AAT GAT TTA CAA GAA AAA TTG AAA GGT GAA TTA GAG CAC AAT CAG | 1537 |
| Ile Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln | |
| 500 505 510 | |
| AAA TTA AAG AAG CAA GCT GTT GAG CTT AGA GTT GCT CAG TCT GCT ACT | 1585 |
| Lys Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr | |
| 515 520 525 | |
| GAA CAA CTG AAT AAT GAA TTA CAG GAA ACT ATG CAG GGT TTA CAA ACA | 1633 |
| Glu Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr | |
| 530 535 540 | |
| CAA AGA GAT GCT TTA CAA CAA GAA GTA GCA TCT CTC CAA GGC AAA CTT | 1681 |
| Gln Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu | |
| 545 550 555 | |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| TCT CAA GAG AGG AGC TCT AGA TCA CAG GCT TCT GAT ATG CAG ATA GAA Ser Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu 560 565 570 575 | 1729 |
| CTA GAA GCA AAA TTG CAG GCT CTC CAT ATT GAA CTG GAG CAT GTC AGA Leu Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg 580 585 590 | 1777 |
| AAT TGT GAA GAC AAA GTT ACC CAA GAC AAC AGA CAA CTA TTG GAA AGG Asn Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg 595 600 605 | 1825 |
| ATA TCA ACA TTG GAG AAA GAA TGT GCT TCT CTA GAA TTA GAA TTG AAA Ile Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys 610 615 620 | 1873 |
| GCA ACA CAA AAC AAA TAT GAG CAA GAG GTC AAA GCA CAT CGC GAA ACT Ala Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr 625 630 635 | 1921 |
| GAA AAA TCA AGA CTG GTC AGT AAA GAA GAA GCA AAT ATG GAG GAA GTT Glu Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val 640 645 650 655 | 1969 |
| AAA GCA CTC CAA ATA AAA TTA AAT GAA GAG AAA TCT GCT CGA CAG AAA Lys Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys 660 665 670 | 2017 |
| TCT GAT CAG AAT TCT CAA GAA AAG GAA CGA CAA ATT TCT ATG TTA TCT Ser Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser 675 680 685 | 2065 |
| GTG GAT TAT CGT CAA ATC CAA CAG CGT TTG CAA AAG CTA GAA GGA GAA Val Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu 690 695 700 | 2113 |
| TAT AGG CAA GAG AGT GAA AAA GTT AAA GCT CTC CAC AGT CAG ATT GAG Tyr Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu 705 710 715 | 2161 |
| CAA GAG CAA CTA AAA AAA TCA CAA TTA CAA AGC GAA TTG GGT GTT CAA Gln Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln 720 725 730 735 | 2209 |
| AGG TCT CAG ACT GCA CAT TTA ACA GCC AGG GAA GCT CAG CTA GTT GGA Arg Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly 740 745 750 | 2257 |
| GAA GTT GCT CAT CTT AGA GAT GCT AAA AGA AAT GTT GAA GAA GAG TTA Glu Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu 755 760 765 | 2305 |
| CAC AAG TTA AAA ACT GCT CGA TCA GTG GAT AAT GCT CAG ATG AAA GAG His Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu 770 775 780 | 2353 |
| CTT CAA GAA CAA GTT GAA GCC GAG CAA GTT TTC TCG ACT CTT TAT AAA Leu Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys | 2401 |

2618-17-C4-PUS-2.txt

| | | | | | |
|---|-----|-----|-----|-----|------|
| 785 | | 790 | | 795 | |
| ACA CAT TCT AAT GAA CTT AAG GAA GAA CTT GAG GAA AAA TCT CGT CAT | | | | | 2449 |
| Thr His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His | | | | | |
| 800 | | 805 | | 810 | 815 |
| ATT CAA GAA ATG GAA GAA GAA AGA GAA AGT TTG GTT CAT CAG CTA CAA | | | | | 2497 |
| Ile Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln | | | | | |
| | 820 | | 825 | | 830 |
| ATT GCA TTA GCT AGA GCT GAT TCA GAG GCA TTG GCG AGA TCA ATA GCT | | | | | 2545 |
| Ile Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala | | | | | |
| | 835 | | 840 | | 845 |
| GAT GAA AGT ATA GCT GAT TTA GAA AAG GAA AAG ACT ATG AAG GAA TTA | | | | | 2593 |
| Asp Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu | | | | | |
| | 850 | | 855 | | 860 |
| GAA CTA AAA GAA TTA TTA AAC AAA AAT CGT ACT GAA CTT TCC CAG AAA | | | | | 2641 |
| Glu Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys | | | | | |
| | 865 | | 870 | | 875 |
| GAC ATT TCA ATA AGT GCA TTG CGT GAA CGA GAA AAT GAA CAG AAG AAA | | | | | 2689 |
| Asp Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys | | | | | |
| 880 | | 885 | | 890 | 895 |
| CTT TTA GAA CAA ATC TC | | | | | 2706 |
| Leu Leu Glu Gln Ile | | | | | |
| | 900 | | | | |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Ile | Glu | Ala | Tyr | Thr | Asn | Arg | Tyr | Glu | Ile | Ile | Ala | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Ile | Val | Asn | Leu | Arg | Met | Lys | Pro | Asp | Asp | Phe | Asn | Leu | Ile | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ile | Gly | Arg | Gly | Ala | Phe | Gly | Glu | Val | Gln | Leu | Val | Arg | His | Lys |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Ser | Thr | Ala | Gln | Val | Phe | Ala | Met | Lys | Arg | Leu | Ser | Lys | Phe | Glu | Met |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Lys | Arg | Pro | Asp | Ser | Ala | Phe | Phe | Trp | Glu | Glu | Arg | His | Ile | Met |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ala | His | Ala | Lys | Ser | Glu | Trp | Ile | Val | Gln | Leu | His | Phe | Ala | Phe | Gln |
| | | | 85 | | | | | 90 | | | | | 95 | | |

2618-17-C4-PUS-2.txt

Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly Asp
 100 105 110
 Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala Met
 115 120 125
 Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser Met
 130 135 140
 Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
 145 150 155 160
 Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asp
 165 170 175
 Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp Tyr
 180 185 190
 Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr Gly
 195 200 205
 Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met Leu
 210 215 220
 Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
 225 230 235 240
 Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val Glu
 245 250 255
 Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp Arg
 260 265 270
 Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His Pro
 275 280 285
 Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser Ala
 290 295 300
 Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn Phe
 305 310 315 320
 Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile Pro
 325 330 335
 Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr Asn
 340 345 350
 Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp Met
 355 360 365
 Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp Val
 370 375 380
 Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu Asn
 385 390 395 400
 Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu Gly

| | | |
|---|-----|-----|
| 405 | 410 | 415 |
| Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys Glu | | |
| 420 | 425 | 430 |
| Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala Glu | | |
| 435 | 440 | 445 |
| Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu Thr | | |
| 450 | 455 | 460 |
| Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met Asn | | |
| 465 | 470 | 475 |
| Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln Ile | | |
| 485 | 490 | 495 |
| Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln Lys | | |
| 500 | 505 | 510 |
| Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr Glu | | |
| 515 | 520 | 525 |
| Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr Gln | | |
| 530 | 535 | 540 |
| Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu Ser | | |
| 545 | 550 | 555 |
| Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu Leu | | |
| 565 | 570 | 575 |
| Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg Asn | | |
| 580 | 585 | 590 |
| Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg Ile | | |
| 595 | 600 | 605 |
| Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys Ala | | |
| 610 | 615 | 620 |
| Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr Glu | | |
| 625 | 630 | 635 |
| Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val Lys | | |
| 645 | 650 | 655 |
| Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys Ser | | |
| 660 | 665 | 670 |
| Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser Val | | |
| 675 | 680 | 685 |
| Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu Tyr | | |
| 690 | 695 | 700 |
| Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu Gln | | |
| 705 | 710 | 715 |
| | | 720 |

Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln Arg
 725 730 735
 Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly Glu
 740 745 750
 Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu His
 755 760 765
 Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu Leu
 770 775 780

 Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys Thr
 785 790 795 800
 His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His Ile
 805 810 815
 Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln Ile
 820 825 830
 Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala Asp
 835 840 845
 Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu Glu
 850 855 860
 Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys Asp
 865 870 875 880
 Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys Leu
 885 890 895
 Leu Glu Gln Ile
 900

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GA GCT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA
 Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly
 1 5 10 15

```

AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT      95
Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr
                20                25                30

GAT GAG AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG      143
Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val
                35                40                45

ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG      191
Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu
                50                55                60

AAT GGA AAT GTG ATT AGC ATT ACT GAT GAG AAT GGA AAT GTG ATT AGC      239
Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser
                65                70                75

ATT ACT GAT GAA AAT GGA AAC TCG AAT AGC ACT ACT AGT GTT TTC AAT      287
Ile Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn
    80                85                90                95

GAA ACT GAA AAT ATG ACT GGT GCT GCT GAT ACA AAT GAA TAT TCA ATT      335
Glu Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile
                100                105                110

GGT TCT ACT GAC GGA AAT GGA AAT TTT ATA AGT ACT TTT AGT GAT CAT      383
Gly Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His
                115                120                125

GAT TAC GTA AGT AAT ACT GAA GAA AAT GAA  A      414
Asp Tyr Val Ser Asn Thr Glu Glu Asn Glu
                130                135

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
 1                5                10                15

Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp
                20                25                30

Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile
                35                40                45

Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn
    50                55                60

Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser Ile

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | 70 | | 75 | | 80 | | | | | | | | | |
| Thr | Asp | Glu | Asn | Gly | Asn | Ser | Asn | Ser | Thr | Thr | Ser | Val | Phe | Asn | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Glu | Asn | Met | Thr | Gly | Ala | Ala | Asp | Thr | Asn | Glu | Tyr | Ser | Ile | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Thr | Asp | Gly | Asn | Gly | Asn | Phe | Ile | Ser | Thr | Phe | Ser | Asp | His | Asp |
| | | 115 | | | | | | 120 | | | | 125 | | | |
| Tyr | Val | Ser | Asn | Thr | Glu | Glu | Asn | Glu | | | | | | | |
| | 130 | | | | | | | 135 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AT | GAG | AAT | GGA | AAT | GTG | ATT | AGC | TAT | ACT | GAT | GAA | AAT | GGA | AAC | ATT | 47 |
| Glu | Asn | Gly | Asn | Val | Ile | Ser | Tyr | Thr | Asp | Glu | Asn | Gly | Asn | Ile | | |
| 1 | | | | 5 | | | | | | 10 | | | | 15 | | |
| ATC | AGT | ACT | ACT | GAT | GAG | AAT | GGA | AAT | GTG | ATT | AGC | ATT | ACT | GAT | GAA | 95 |
| Ile | Ser | Thr | Thr | Asp | Glu | Asn | Gly | Asn | Val | Ile | Ser | Ile | Thr | Asp | Glu | |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| AAT | GGA | AAT | GTG | ATT | AGC | ATT | ACT | GAT | GAA | AAT | GGA | AAC | ATT | ATC | AGT | 143 |
| Asn | Gly | Asn | Val | Ile | Ser | Ile | Thr | Asp | Glu | Asn | Gly | Asn | Ile | Ile | Ser | |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| ACT | ACT | GAT | GAG | AAT | GGA | AAT | GTG | ATT | AGC | ATT | ACT | GAT | GAA | AAT | GGA | 191 |
| Thr | Thr | Asp | Glu | Asn | Gly | Asn | Val | Ile | Ser | Ile | Thr | Asp | Glu | Asn | Gly | |
| | | | 50 | | | | 55 | | | | | 60 | | | | |
| AAT | GTG | ATT | AGC | ATT | ACT | GAT | GAA | AAT | GGA | AAC | ATT | ATT | AGT | ACT | ACT | 239 |
| Asn | Val | Ile | Ser | Ile | Thr | Asp | Glu | Asn | Gly | Asn | Ile | Ile | Ser | Thr | Thr | |
| | 65 | | | | | 70 | | | | | 75 | | | | | |
| GAT | GAG | AAT | GGA | AAT | GTG | ATT | AGC | AAT | ACT | CGA | G | | | | | 273 |
| Asp | Glu | Asn | Gly | Asn | Val | Ile | Ser | Asn | Thr | Arg | | | | | | |
| 80 | | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile Ile
 1             5             10             15
Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn
      20             25             30
Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr
      35             40             45
Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
      50             55             60
Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp
      65             70             75             80
Glu Asn Gly Asn Val Ile Ser Asn Thr Arg
      85             90

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 24..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

CAGAAACCCG ACATTCTCAA AAT ATG GAA CCT CAA TCG CTG TCT TGG CAA      50
              Met Glu Pro Gln Ser Leu Ser Trp Gln
              1             5
CTT CCG ACT CAA GTA GTT CAG CCA GTT TTT GAA CAA CAA ATG CAG ATT      98
Leu Pro Thr Gln Val Val Gln Pro Val Phe Glu Gln Gln Met Gln Ile
 10             15             20             25
CCT GGA TAT AAT ATG CAA ATT CAA TCT AAT TAT TAT CAA ATT CAC CCA      146
Pro Gly Tyr Asn Met Gln Ile Gln Ser Asn Tyr Tyr Gln Ile His Pro
      30             35             40
GAA ATG TTG GAT CCA AAT TTG AAC AAT CCT CAG CAG TTA ATG TTT AAT      194
Glu Met Leu Asp Pro Asn Leu Asn Asn Pro Gln Gln Leu Met Phe Asn

```

2618-17-C4-PUS-2.txt

| 45 | | | | | | | | | | 50 | | | | | 55 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| TAT | ATG | CAA | TTA | CAA | CAA | TTG | CAG | GAA | CTA | CAA | CAT | TTA | AGT | CAA | CAA | 242 | | | | |
| Tyr | Met | Gln | Leu | Gln | Gln | Leu | Gln | Glu | Leu | Gln | His | Leu | Ser | Gln | Gln | | | | | |
| 60 | | | | | | 65 | | | | | 70 | | | | | | | | | |
| CAG | CCA | ATG | CAT | CAT | GAA | TTT | GAA | CAT | CAT | ATC | CCC | ATT | CCA | CAA | GAA | 290 | | | | |
| Gln | Pro | Met | His | His | Glu | Phe | Glu | His | His | Ile | Pro | Ile | Pro | Gln | Glu | | | | | |
| 75 | | | | | | 80 | | | | | 85 | | | | | | | | | |
| GCA | ACT | TCA | ACT | AAT | TAC | GGT | CCA | TCC | GGA | CAG | TAT | ATT | ACT | AGT | GAC | 338 | | | | |
| Ala | Thr | Ser | Thr | Asn | Tyr | Gly | Pro | Ser | Gly | Gln | Tyr | Ile | Thr | Ser | Asp | | | | | |
| 90 | | | | | | 95 | | | | | 100 | | | | 105 | | | | | |
| GCA | ACA | TCT | TAT | CAA | TCA | ATT | GCC | CAA | CAA | TTT | GTA | CCA | CAA | CCA | CCA | 386 | | | | |
| Ala | Thr | Ser | Tyr | Gln | Ser | Ile | Ala | Gln | Gln | Phe | Val | Pro | Gln | Pro | Pro | | | | | |
| 110 | | | | | | 115 | | | | | 120 | | | | | | | | | |
| ATT | GAA | ACT | ACC | ACC | ACG | AAA | ATA | CCT | GAA | ACT | GAA | ATT | CAA | ATT | GGC | 434 | | | | |
| Ile | Glu | Thr | Thr | Thr | Thr | Lys | Ile | Pro | Glu | Thr | Glu | Ile | Gln | Ile | Gly | | | | | |
| 125 | | | | | | 130 | | | | | 135 | | | | | | | | | |
| GTT | TCG | AAT | CAA | TAT | GCC | CAA | AAT | ATA | ACT | TAT | AAT | TCA | AAT | ATC | AGT | 482 | | | | |
| Val | Ser | Asn | Gln | Tyr | Ala | Gln | Asn | Ile | Thr | Tyr | Asn | Ser | Asn | Ile | Ser | | | | | |
| 140 | | | | | | 145 | | | | | 150 | | | | | | | | | |
| CCT | GAA | GTG | ATT | GGA | TTC | CGA | GAA | CAT | TAT | GTT | GCG | GAA | CAG | CCT | TCT | 530 | | | | |
| Pro | Glu | Val | Ile | Gly | Phe | Arg | Glu | His | Tyr | Val | Ala | Glu | Gln | Pro | Ser | | | | | |
| 155 | | | | | | 160 | | | | | 165 | | | | | | | | | |
| GGT | GAC | GTG | CTT | CAC | AAA | AGT | CAT | TTA | ACA | GAA | CAA | CCA | GCA | GAT | AAA | 578 | | | | |
| Gly | Asp | Val | Leu | His | Lys | Ser | His | Leu | Thr | Glu | Gln | Pro | Ala | Asp | Lys | | | | | |
| 170 | | | | | | 175 | | | | | 180 | | | | 185 | | | | | |
| AGC | ACA | CGT | GGT | GAT | CAG | GAA | CCT | GTT | AGT | GAG | ACA | GGC | TCT | GGT | TTT | 626 | | | | |
| Ser | Thr | Arg | Gly | Asp | Gln | Glu | Pro | Val | Ser | Glu | Thr | Gly | Ser | Gly | Phe | | | | | |
| 190 | | | | | | 195 | | | | | 200 | | | | | | | | | |
| TCG | TAT | GCA | CAA | ATT | TTA | TCA | CAG | GGA | CTT | AAG | CCT | ACC | CAG | CCA | TCC | 674 | | | | |
| Ser | Tyr | Ala | Gln | Ile | Leu | Ser | Gln | Gly | Leu | Lys | Pro | Thr | Gln | Pro | Ser | | | | | |
| 205 | | | | | | 210 | | | | | 215 | | | | | | | | | |
| AAC | TCA | GTT | AAT | TTG | CTT | GCA | GAT | CGA | TCG | AGA | TCA | CCT | CTA | GAT | ACG | 722 | | | | |
| Asn | Ser | Val | Asn | Leu | Leu | Ala | Asp | Arg | Ser | Arg | Ser | Pro | Leu | Asp | Thr | | | | | |
| 220 | | | | | | 225 | | | | | 230 | | | | | | | | | |
| AAA | ACG | AAA | GAA | AAT | TAT | AAA | TCT | CCT | GGT | CGT | GTG | CAG | GAT | ATC | ACG | 770 | | | | |
| Lys | Thr | Lys | Glu | Asn | Tyr | Lys | Ser | Pro | Gly | Arg | Val | Gln | Asp | Ile | Thr | | | | | |
| 235 | | | | | | 240 | | | | | 245 | | | | | | | | | |
| AAA | ATA | ATA | GAT | GAG | AAA | CAA | AAG | TCG | TCA | AAA | GAC | ACA | GAG | TGG | CAT | 818 | | | | |
| Lys | Ile | Ile | Asp | Glu | Lys | Gln | Lys | Ser | Ser | Lys | Asp | Thr | Glu | Trp | His | | | | | |
| 250 | | | | | | 255 | | | | | 260 | | | | 265 | | | | | |
| AAT | AAG | AAA | GTG | AAA | GAA | CAT | AAA | AAA | GTG | AAA | GAT | ATC | AAA | CCT | GAT | 866 | | | | |
| Asn | Lys | Lys | Val | Lys | Glu | His | Lys | Lys | Val | Lys | Asp | Ile | Lys | Pro | Asp | | | | | |
| 270 | | | | | | 275 | | | | | 280 | | | | | | | | | |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| TTC GAA TCT TCT CAA AGG AAT AAG AAA AGC AAG AAT ATT CCT AAG CAA | 914 |
| Phe Glu Ser Ser Gln Arg Asn Lys Lys Ser Lys Asn Ile Pro Lys Gln | |
| 285 290 295 | |
| ATT GAA AAT ATC ACA CCT CAA CTT GAC AGC TTA CGA TCA CGA GAT ATA | 962 |
| Ile Glu Asn Ile Thr Pro Gln Leu Asp Ser Leu Arg Ser Arg Asp Ile | |
| 300 305 310 | |
| GTA ATT AAG GGA GAA TTA CTA ACA AAA GAT ACT ACA AAA AGT TTA ACT | 1010 |
| Val Ile Lys Gly Glu Leu Thr Lys Asp Thr Thr Lys Ser Leu Thr | |
| 315 320 325 | |
| ACT GTT AAT GTT GAT AGT GAA TTA GAT AGT GTA AAA CCT AAA GAT GAA | 1058 |
| Thr Val Asn Val Asp Ser Glu Leu Asp Ser Val Lys Pro Lys Asp Glu | |
| 330 335 340 345 | |
| AAA CCT GAA CCT TCT GAA CCT AGT AAA ACG TTT ATT GAT ACT TCA GTT | 1106 |
| Lys Pro Glu Pro Ser Glu Pro Ser Lys Thr Phe Ile Asp Thr Ser Val | |
| 350 355 360 | |
| GCA AAG GAT GTT GAT AAT TCT ACA CAG GCG AAC CAT AAA AAG AAG AAA | 1154 |
| Ala Lys Asp Val Asp Asn Ser Thr Gln Ala Asn His Lys Lys Lys Lys | |
| 365 370 375 | |
| AGT AAA TCT AAG CCG AGG AAA ACG GAA CCG GAA GAT GAA ATT GAA AAA | 1202 |
| Ser Lys Ser Lys Pro Arg Lys Thr Glu Pro Glu Asp Glu Ile Glu Lys | |
| 380 385 390 | |
| GCT TTG AAA GAA ATT CAA GCT AGT GAG AAA AAA CTT ACG AAG TCT ATC | 1250 |
| Ala Leu Lys Glu Ile Gln Ala Ser Glu Lys Lys Leu Thr Lys Ser Ile | |
| 395 400 405 | |
| GAT AAC ATT GTG AAT AAA TTT AAT ACA CCA CTT GCT AGT GTT AAA GCC | 1298 |
| Asp Asn Ile Val Asn Lys Phe Asn Thr Pro Leu Ala Ser Val Lys Ala | |
| 410 415 420 425 | |
| GAT GAT TCC AAT TCT ACC AAG GAT AAT GTA CCA GCA AAG AAG AAA AAA | 1346 |
| Asp Asp Ser Asn Ser Thr Lys Asp Asn Val Pro Ala Lys Lys Lys Lys | |
| 430 435 440 | |
| CCT TCG AAG TCA TCT GTT TCT TTA CCT GAG AAT GTA GTA CAA AAT CTA | 1394 |
| Pro Ser Lys Ser Ser Val Ser Leu Pro Glu Asn Val Val Gln Asn Leu | |
| 445 450 455 | |
| TTG ATA CTA ACA TAA CTACTAGTAG CGACAAGATT GAAAACATGC CGCAACCGCA | 1449 |
| Leu Ile Leu Thr | |
| 460 | |
| ACCAAAAAGA GAAGATTTAC AAGATGCAGC TAAGGAAGTA TTGACTTCAA TAGAGTCAGT | 1509 |
| AATGATGCAG TCTGTTGAGA CTATTCCTAT TACGAAGAAA AGAGTAAATA AGAAAAAGAA | 1569 |
| TACCACTCAA CAGACGAAGG AATTTGTGGA ACACGAAATA TGCGATACAT CAAAAAATGA | 1629 |
| AACTTTAAAA AATATTGAAA AAGAATCGCA TGAGAATATG GCTATATTGC AAACAAGTCC | 1689 |
| GAAACCGCCA CTAAG | 1704 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Glu Pro Gln Ser Leu Ser Trp Gln Leu Pro Thr Gln Val Val Gln
 1             5             10             15
Pro Val Phe Glu Gln Gln Met Gln Ile Pro Gly Tyr Asn Met Gln Ile
      20             25             30
Gln Ser Asn Tyr Tyr Gln Ile His Pro Glu Met Leu Asp Pro Asn Leu
      35             40             45
Asn Asn Pro Gln Gln Leu Met Phe Asn Tyr Met Gln Leu Gln Gln Leu
      50             55             60
Gln Glu Leu Gln His Leu Ser Gln Gln Gln Pro Met His His Glu Phe
 65             70             75             80
Glu His His Ile Pro Ile Pro Gln Glu Ala Thr Ser Thr Asn Tyr Gly
      85             90             95
Pro Ser Gly Gln Tyr Ile Thr Ser Asp Ala Thr Ser Tyr Gln Ser Ile
      100            105            110
Ala Gln Gln Phe Val Pro Gln Pro Pro Ile Glu Thr Thr Thr Thr Lys
      115            120            125
Ile Pro Glu Thr Glu Ile Gln Ile Gly Val Ser Asn Gln Tyr Ala Gln
      130            135            140
Asn Ile Thr Tyr Asn Ser Asn Ile Ser Pro Glu Val Ile Gly Phe Arg
      145            150            155            160
Glu His Tyr Val Ala Glu Gln Pro Ser Gly Asp Val Leu His Lys Ser
      165            170            175
His Leu Thr Glu Gln Pro Ala Asp Lys Ser Thr Arg Gly Asp Gln Glu
      180            185            190
Pro Val Ser Glu Thr Gly Ser Gly Phe Ser Tyr Ala Gln Ile Leu Ser
      195            200            205
Gln Gly Leu Lys Pro Thr Gln Pro Ser Asn Ser Val Asn Leu Leu Ala
      210            215            220
Asp Arg Ser Arg Ser Pro Leu Asp Thr Lys Thr Lys Glu Asn Tyr Lys
      225            230            235            240
Ser Pro Gly Arg Val Gln Asp Ile Thr Lys Ile Ile Asp Glu Lys Gln
      245            250            255

```


Lys Ser Ser Lys Asp Thr Glu Trp His Asn Lys Lys Val Lys Glu His
 260 265 270
 Lys Lys Val Lys Asp Ile Lys Pro Asp Phe Glu Ser Ser Gln Arg Asn
 275 280 285
 Lys Lys Ser Lys Asn Ile Pro Lys Gln Ile Glu Asn Ile Thr Pro Gln
 290 295 300
 Leu Asp Ser Leu Arg Ser Arg Asp Ile Val Ile Lys Gly Glu Leu Leu
 305 310 315 320
 Thr Lys Asp Thr Thr Lys Ser Leu Thr Thr Val Asn Val Asp Ser Glu
 325 330 335
 Leu Asp Ser Val Lys Pro Lys Asp Glu Lys Pro Glu Pro Ser Glu Pro
 340 345 350
 Ser Lys Thr Phe Ile Asp Thr Ser Val Ala Lys Asp Val Asp Asn Ser
 355 360 365
 Thr Gln Ala Asn His Lys Lys Lys Lys Ser Lys Ser Lys Pro Arg Lys
 370 375 380
 Thr Glu Pro Glu Asp Glu Ile Glu Lys Ala Leu Lys Glu Ile Gln Ala
 385 390 395 400
 Ser Glu Lys Lys Leu Thr Lys Ser Ile Asp Asn Ile Val Asn Lys Phe
 405 410 415
 Asn Thr Pro Leu Ala Ser Val Lys Ala Asp Asp Ser Asn Ser Thr Lys
 420 425 430
 Asp Asn Val Pro Ala Lys Lys Lys Lys Pro Ser Lys Ser Ser Val Ser
 435 440 445
 Leu Pro Glu Asn Val Val Gln Asn Leu Leu Ile Leu Thr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| ATGGAACCTC AATCGCTGTC TTGGCAACTT CCGACTCAAG TAGTTCAGCC AGTTTTTGAA | 60 |
| CAACAAATGC AGATTCCTGG ATATAATATG CAAATTCAAT CTAATTATTA TCAAATTCAC | 120 |
| CCAGAAATGT TGGATCCAAA TTTGAACAAT CCTCAGCAGT TAATGTTTAA TTATATGCAA | 180 |

2618-17-C4-PUS-2.txt

| | |
|--|------|
| TTACAACAAT TGCAGGAAC TACAACATTTA AGTCAACAAC AGCCAATGCA TCATGAATTT | 240 |
| GAACATCATA TCCCCATTCC ACAAGAAGCA ACTTCAACTA ATTACGGTCC ATCCGGACAG | 300 |
| TATATTACTA GTGACGCAAC ATCTTATCAA TCAATTGCCC AACAAATTTGT ACCACAACCA | 360 |
| CCAATTGAAA CTACCACCAC GAAAATACCT GAAACTGAAA TTCAAATTGG CGTTTCGAAT | 420 |
| CAATATGCCC AAAATATAAC TTATAATTCA AATATCAGTC CTGAAGTGAT TGGATTCCGA | 480 |
| GAACATTATG TTGCGGAACA GCCTTCTGGT GACGTGCTTC ACAAAAGTCA TTTAACAGAA | 540 |
| CAACCAGCAG ATAAAAGCAC ACGTGGTGAT CAGGAACCTG TTAGTGAGAC AGGCTCTGGT | 600 |
| TTTTTCGTATG CACAAATTTT ATCACAGGGA CTTAAGCCTA CCCAGCCATC CAACTCAGTT | 660 |
| AATTTGCTTG CAGATCGATC GAGATCACCT CTAGATACGA AAACGAAAGA AAATTATAAA | 720 |
| TCTCCTGGTC GTGTGCAGGA TATCACGAAA ATAATAGATG AGAAACAAAA GTCGTCAAAA | 780 |
| GACACAGAGT GGCATAATAA GAAAGTGAAA GAACATAAAA AAGTGAAAGA TATCAAACCT | 840 |
| GATTTCGAAT CTTCTCAAAG GAATAAGAAA AGCAAGAATA TTCCTAAGCA AATTGAAAT | 900 |
| ATCACACCTC AACTTGACAG CTTACGATCA CGAGATATAG TAATTAAGGG AGAATTACTA | 960 |
| ACAAAAGATA CTACAAAAAG TTAACTACT GTTAATGTTG ATAGTGAATT AGATAGTGTA | 1020 |
| AAACCTAAAG ATGAAAAACC TGAACCTTCT GAACCTAGTA AAACGTTTAT TGATACTTCA | 1080 |
| GTTGCAAAGG ATGTTGATAA TTCTACACAG GCGAACCATA AAAAGAAGAA AAGTAAATCT | 1140 |
| AAGCCGAGGA AAACGGAACC GGAAGATGAA ATTGAAAAAG CTTTGAAAGA AATTCAAGCT | 1200 |
| AGTGAGAAAA AACTTACGAA GTCTATCGAT AACATTGTGA ATAAATTTAA TACACCACTT | 1260 |
| GCTAGTGTTA AAGCCGATGA TTCCAATTCT ACCAAGGATA ATGTACCAGC AAAGAAGAAA | 1320 |
| AAACCTTCGA AGTCATCTGT TTCTTTACCT GAGAATGTAG TACAAAATCT ATTGATACTA | 1380 |
| ACA | 1383 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...1758

(ix) FEATURE:

(A) NAME/KEY: W = A or T

(B) LOCATION: 1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| CTA GAG ATG GCT AAA TTT CTG ACG GAA ACA TTA GAC GAC ATG ACT CTA | 48 |
| Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu | |
| 1 5 10 15 | |
| CAA CAC AAA GAT CAC AGA TCA GAA TTG GCT AAA GAG TTT TCA ATT TGG | 96 |
| Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp | |
| 20 25 30 | |
| TTT ACG AAA ATG AGA CAG TCT GGC GCT CAA GCC AGT AAC GAA GAA ATC | 144 |
| Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile | |
| 35 40 45 | |
| ATG AAA TTT TCA AAA TTG TTT GAA GAT GAA ATC ACT CTT GAC TCG CTG | 192 |
| Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu | |
| 50 55 60 | |
| GCG AGG CCG CAA CTT GTT GCT TTG TGC AGG GTA CTA GAA ATC AGT ACT | 240 |
| Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr | |
| 65 70 75 80 | |
| TTA GGA ACA ACA AAT TTC TTA AGG TTT CAA CTG CGA ATG AAA CTG CGT | 288 |
| Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg | |
| 85 90 95 | |
| TCA TTA GCT GCT GAT GAT AAA ATG ATT CAA AAA GAA GGC ATA GTT TCT | 336 |
| Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser | |
| 100 105 110 | |
| ATG ACT TAT TCG GAG GTG CAA CAG GCC TGC AGA GCT CGT GGA ATG CGA | 384 |
| Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg | |
| 115 120 125 | |
| GCT TAT GGT ATG CCT GAA CAT AGG TTG AGG AGG CAA TTG GAA GAC TGG | 432 |
| Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp | |
| 130 135 140 | |
| ATT AAT TTA AGC TTG AAT GAA AAG GTT CCA CCA TCA TTA TTG CTT TTG | 480 |
| Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu | |
| 145 150 155 160 | |
| TCA AGG GCG CTG ATG TTG CCC GAG AAT GTT CCA GTG TCT GAT AAA CTT | 528 |
| Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu | |
| 165 170 175 | |
| AAA GCA ACA ATA AAT GCT CTT CCT GAA ACT ATT GTA ACT CAG ACA AAG | 576 |
| Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys | |
| 180 185 190 | |
| GCT GCT ATT GGA GAA AGA GAA GGA AAG ATT GAC AAT AAG ACC AAA ATT | 624 |
| Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile | |
| 195 200 205 | |
| GAG GTC ATC AAA GAG GAA GAA CGC AAA ATT CGC GAA GAG CGC CAA GAA | 672 |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu | |
| 210 215 220 | |
| GCA CGT GAG GAA GAG GAA CAA CGC AAG CAA GCC GAA CTT GCT CTT AAT | 720 |
| Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn | |
| 225 230 235 240 | |
| GCC AGT TCT GCA GCA GCT GAG GCC TCT TCA GCT CAG GAA CTT TTG ATA | 768 |
| Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile | |
| 245 250 255 | |
| GAT ACA GCT CCT GTA ATA GAT GCA GAA AAG ACA CCA AAG GTG GCA ACA | 816 |
| Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr | |
| 260 265 270 | |
| TCA CCT GTT GAA TCA CCA TTG GCA CCA CCA GAA GTT CTG ATT ATG GGT | 864 |
| Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly | |
| 275 280 285 | |
| GCT CCT AAA ACA CCT GTT GCA ACC GAA GTG GAT AAG AAT GCT GAT GAG | 912 |
| Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu | |
| 290 295 300 | |
| GTG GAA TTC ACC AAG AAA GAT CTT GAG GTT GTT GAA GAT GCA TTG GAT | 960 |
| Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp | |
| 305 310 315 320 | |
| ACA CTA TCG AAA GAC AAA AAT AAT TTG GTG ATT GAA AAG GAA GTT ATT | 1008 |
| Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile | |
| 325 330 335 | |
| AAA GAC ATT AAG GAA GAA ATT GCT GAT TAC CAA GAA GAT GTA GAA GAA | 1056 |
| Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu | |
| 340 345 350 | |
| TTG AAA GAA GCC ATA GTT GCT GCT GAG AAA CCA AAG GAT GAG ATA AAA | 1104 |
| Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys | |
| 355 360 365 | |
| GAA ACT AAA GGA GCT CAA CGA TTG TTG AAG AAG GTT AAC AAG ATG ATA | 1152 |
| Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile | |
| 370 375 380 | |
| ACG AAA ATG GAT ACT GTT GTA CAA GAA ATT GAA AGC AAA GAA TCT GAG | 1200 |
| Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu | |
| 385 390 395 400 | |
| AAG AAA GCC AAA ACA TTG CCA CTT GAA GCT CCT AGG AGC GCT ACT GAA | 1248 |
| Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu | |
| 405 410 415 | |
| ACT CAA GAA TTA GAT GTA AGG AAA GAA AGA GGA GAG ATT TTA ATT GAC | 1296 |
| Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp | |
| 420 425 430 | |
| GAA TTA ATG GAC GCT ATT AAG AAA GTT AAA AAT GTG CCA GAC GAA AAT | 1344 |
| Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn | |
| 435 440 445 | |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| CGC TTG AAA TTA ATT GAG AAC ATT TTG GGC AGG ATC GAT ACT GAC AAA | 1392 |
| Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys | |
| 450 455 460 | |
| GAT AGG CAT ATC AAA GTT GAA GAT GTA TTG AAG GTT ATT GAC ATT GTG | 1440 |
| Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val | |
| 465 470 475 480 | |
| GAA AAA GAA GAT GGT ATC ATG AGT ACA AAA CAA TTA GAT GAG TTG GTT | 1488 |
| Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val | |
| 485 490 495 | |
| CAG CTT TTG AAA AAG GAG GAA GTT ATT GAA TTG GAA GAA AAG AAA GAA | 1536 |
| Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu | |
| 500 505 510 | |
| AAG CAA GAG TCT CAA CAG AAA AGT TTT GTA CCA CCA AGT GAA ACT TTG | 1584 |
| Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu | |
| 515 520 525 | |
| CAT CTT GAA TCA TCA CAG CAG AAG AGT ACA GTT CCT AGC TCG GGA CAT | 1632 |
| His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His | |
| 530 535 540 | |
| GAA GCT AAG GTG TCC GAA GAT GAC TTA AAT GTT AAA AAT AAA AAT TTG | 1680 |
| Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu | |
| 545 550 555 560 | |
| GAA GAA TCG ACC AAA ACT GAA TGT GGA GCA ATT GAC GAA GAG CAC AGA | 1728 |
| Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg | |
| 565 570 575 | |
| AGA GAG CAT TGC CAG TAC CCA GAC ATT ACA | 1758 |
| Arg Glu His Cys Gln Tyr Pro Asp Ile Thr | |
| 580 585 | |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|---|--|
| Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu | |
| 1 5 10 15 | |
| Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp | |
| 20 25 30 | |
| Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile | |
| 35 40 45 | |
| Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu | |
| 50 55 60 | |

2618-17-C4-PUS-2.txt

Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
 65 70 75 80
 Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
 85 90 95
 Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
 100 105 110
 Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg
 115 120 125
 Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
 130 135 140
 Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu
 145 150 155 160
 Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
 165 170 175
 Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
 180 185 190
 Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
 195 200 205
 Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
 210 215 220
 Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
 225 230 235 240
 Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
 245 250 255
 Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
 260 265 270
 Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
 275 280 285
 Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
 290 295 300
 Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
 305 310 315 320
 Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
 325 330 335
 Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu
 340 345 350
 Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys
 355 360 365
 Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile

```

370                               375                               380
Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu
385                               390                               395                               400
Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu
                               405                               410                               415
Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp
                               420                               425                               430
Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn
                               435                               440                               445
Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys
                               450                               455                               460

Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val
465                               470                               475                               480
Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val
                               485                               490                               495
Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu
                               500                               505                               510
Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu
                               515                               520                               525
His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His
                               530                               535                               540
Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu
545                               550                               555                               560
Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg
                               565                               570                               575
Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
                               580                               585

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

CCCGGGCTGC AGGAATTCGG CACGAGATGA GAATGGAAAT GTGATTAGCT ATACTGATGA      60
AAATGGAAAC ATTATCAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA TTACTGATGA      120

```

2618-17-C4-PUS-2.txt

| | |
|---|-----|
| AAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAC ATTATCAGTA CTACTGATGA | 180 |
| GAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAT GTGATTAGCA TTACTGATGA | 240 |
| AAATGGAAAC ATTATTAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA ATA | 293 |

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | |
|---|-----|
| TTGGAAACAG CTATGACCAT GATTACCCCA AGCTCGAAAG TTAAVCCCTC ACTHARAGGG | 60 |
| GAACAAAAGT CTGGAGCTCC ACCCGCGGAT GCGGCGCCGB TCTAGAACCT AGTGGACTCC | 120 |
| CCCGSGCTG CAGGAATTCG GGCACGAGCT CCAGCTAGCC ATATACATTC ATCCAAAATG | 180 |
| AAGTTGSAAT GTGTCCTACC CGGCAACGGG ATGCCAGAAA TTGKTCGAA ATKTGTGGAC | 240 |
| GAGCACAAGC TTCGTGTCTK TCTATGAAAA ACGTATGGGA GCAGAAGTCG AGGGCCGACA | 300 |
| TCCTCGGCGA TGAATGGARA GGTATGTGC TCCGA | 335 |

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | |
|---|-----|
| ATAGCTTTTA ATATTTTAA TTGATGTATT GCTCAATGGT GATTTCTGTT TATTAACTG | 60 |
| AGTTACCAAT ATGCTCGCTT CAATAGACAT AGCAAATGAA AGCATTCCGT ATCCTCAAGC | 120 |
| GTTACCAAAC TAACATTAAG GAGTTAAATA AATGTTGTTT CCAATAAATA TAATGGGAAA | 180 |
| AACATTTAAT ATTTGTTCCA ATTTGTATTT ATTTTACTA CAATTATATA CAATAAAATA | 240 |
| TTTTTATATA TATTTTATAA AGTTTATGAT GCAGGAGAGA AAATAATGTT AAGAATATAG | 300 |
| GTAATGTGTA TATATAAATG TTTGACAAGC ATGTTCTAGT TAAATAATAA ATACAATGTT | 360 |
| AAATCTACTT AAAAAAAAAA AAAAAAAAAA AAAAAA | 396 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GGAAAGCGAA GAATGAAAAG GGGAAACAAA AAAAGAAAAG ACGAAGGAGT GGAGAGATAA      60
AACGGAGGCA AAGAAGAAAA TGAGGATGCA AAAGAAAGGT AATAAAAGAG ATGAAAAGAA      120
GGAAAAAGGA AATAAGAAAG AAAGAGTGAG GGAAAAATAA AGACAGAGGC GAAGCAAAAA      180
AGGAGGAGAA ATAGAGATTA AAAAAGAAAT ACAGCGAAGA AACCAGGAAA GCGATAAAGA      240
AAAAAAAAGA AAAAAAGAGA GCAGTGAAAA AAAAAAAAAA AAAAAA      285

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

CAGATATTTA CTAAAYATTG TGAAAYAAAT CATTTTCAAA ATGGTSTCCA AAGTGTTTGT      60
TGCTCTTGCC ATCAATGGCT TTATAGGGGG CTSCACAAGY CTTTTTTCGA ACAAGATGMC      120
GTCTTAGATA ASATSGTAGA TRACATCTCT GRCTSMATAT GAGAACARCA TTGSMAGAAT      180
TAGCCAAGGR TNGCRAAATT GATATGMTTS CYGCTGTAAT TCGAAAAA      228

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | |
|---|-----|
| CTT CGT GTC AAC CGC TGG GTC AGA CCT GTT ATT GCT ATG CAC CCA ACC | 48 |
| Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr | |
| 1 5 10 15 | |
| ATG ACT CTT GCT GAA CGT CTC GGC AAA AAA GCT TTG CGC GAC CAA TAT | 96 |
| Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr | |
| 20 25 30 | |
| GCT CCC GTT TGC TCC ATT GGA CAA CGT AAC ATC AAC ACC TTT GAC AAC | 144 |
| Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn | |
| 35 40 45 | |
| ATG ACC TTC CCC GCT CAA TTC GGA AAA TGC TGG CAC GCT TTG TTG CAA | 192 |
| Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln | |
| 50 55 60 | |
| ACT GTT CCC CAA AAG TAT TCC GAA GAA CGT GAA TAC AGC GAA GAA CAA | 240 |
| Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln | |
| 65 70 75 80 | |
| CAA TAC GAC CGT CAA ATG TCC GTC CTC GTT CGT GAA AAC GGC GAA GAA | 288 |
| Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu | |
| 85 90 95 | |
| AAA AGA CGT TAT GAT TGT CTT GGG CAA CCG TTA CAA CAA TTG AAT TGC | 336 |
| Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys | |
| 100 105 110 | |
| AAT | 339 |
| Asn | |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| |
|---|
| Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr |
| 1 5 10 15 |
| Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr |
| 20 25 30 |

2618-17-C4-PUS-2.txt

Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn
 35 40 45

Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln
 50 55 60

Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln
 65 70 75 80

Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu
 85 90 95

Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys
 100 105 110

Asn

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | |
|---|-----|
| TCC AGC TCC TCC AGC TCC AGC AGT GAC TCT TCC AGC TCC AGC AGC TCT | 48 |
| Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser | |
| 1 5 10 15 | |
| TCC TCT TCC AGC TCC AGC AGC TCC TCT TCT GAA TCT TCC GAA GAA AAA | 96 |
| Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys | |
| 20 25 30 | |
| ACC TCC CAC AAA AAA TCC GAA AAG AAG GAA CAC AAA TCC TGC TCC ATC | 144 |
| Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile | |
| 35 40 45 | |
| AAG AAG CAA GTA CAA TTC GTA GAA AAA GAC GGT AAA CTC TGC TTC AGC | 192 |
| Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser | |
| 50 55 60 | |
| ATC CGT CCC TTG GCC GCT TGC CAA AAA CAC TGC AAA GCC ACT GAA ACC | 240 |
| Ile Arg Pro Leu Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr | |
| 65 70 75 80 | |
| ACT CAA ATG GAA GTC GAA GTA TAC TGC CCC TCT GGC AGC CTT GCT GAA | 288 |
| Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu | |
| 85 90 95 | |
| CTT TAC AAA CAA AAG ATC CTT AAG GGA GCC AAC CCC GAC TTG AGC GAC | 336 |

2618-17-C4-PUS-2.txt

| | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----|
| Leu | Tyr | Lys | Gln | Lys | Ile | Leu | Lys | Gly | Ala | Asn | Pro | Asp | Leu | Ser | Asp | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| AAG | ACT | CCT | TCC | AGA | ATC | TTG | AAA | TTC | AAG | GTT | CCC | AAA | GCT | TGC | ACC | | 384 |
| Lys | Thr | Pro | Ser | Arg | Ile | Leu | Lys | Phe | Lys | Val | Pro | Lys | Ala | Cys | Thr | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | |
| GCT | TAC | TAAATCTGAA | ATAAATTACA | TGGATTAGTT | CATTTCTGAT | GTAGTGCAAT | | | | | | | | | | | 440 |
| Ala | Tyr | | | | | | | | | | | | | | | | |
| | | | 130 | | | | | | | | | | | | | | |
| TAGTTCGATA | ATAAATTATT | CAATGAGCAT | TTAAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | AAAAA | 493 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Asp | Ser | Ser | Ser | Ser | Ser | Ser | Ser | |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Glu | Ser | Ser | Glu | Glu | Lys | |
| | | | 20 | | | | | | 25 | | | | | 30 | | | |
| Thr | Ser | His | Lys | Lys | Ser | Glu | Lys | Lys | Glu | His | Lys | Ser | Cys | Ser | Ile | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Lys | Lys | Gln | Val | Gln | Phe | Val | Glu | Lys | Asp | Gly | Lys | Leu | Cys | Phe | Ser | | |
| | 50 | | | | 55 | | | | | 60 | | | | | | | |
| Ile | Arg | Pro | Leu | Ala | Ala | Cys | Gln | Lys | His | Cys | Lys | Ala | Thr | Glu | Thr | | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | | |
| Thr | Gln | Met | Glu | Val | Glu | Val | Tyr | Cys | Pro | Ser | Gly | Ser | Leu | Ala | Glu | | |
| | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Leu | Tyr | Lys | Gln | Lys | Ile | Leu | Lys | Gly | Ala | Asn | Pro | Asp | Leu | Ser | Asp | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Lys | Thr | Pro | Ser | Arg | Ile | Leu | Lys | Phe | Lys | Val | Pro | Lys | Ala | Cys | Thr | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | |
| Ala | Tyr | | | | | | | | | | | | | | | | |
| | | | 130 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

GTAGTGCCAT CATTTCGTAAA CSTTYTGACG GTKGGGCGCT GTATWGGTGC TGCCTGGAAA      60
TTGCATCGAT GCACTWCCGT GTCGGGCGCA WATAGTGCKK TGGSCCCTGT CTGMTTATAG      120
ACATTCAGGG CGCSGGS AKT AGCCATGTTC ATGGCTCMCA AWMTGCAATC ACAGTGGGGT      180
CACATTTT CAG TCGCATGATT KMTCAARTTA GTATMWGADA TATATTTTTTA TCATACTAAG      240
TAGTGAGCDA ATAACACGCG ARWWACRAAC ACCGAATATC TTKAGTTTTT GCACAGATAT      300
KTGTAA                                           306

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

ACCGGATACG TTGCCAATGA CTACGTCACC ACCAATGTTG TTTCCACTCC AGTTACTGGA      60
TACACCACCG GACATCTTGC TAATGACTAC GTCACCACCA ATGTTGTATC CACTCCAGTT      120
ACTGGATACA CCACCGGACA TCTTGCCAAT GACTACGTCA CCACCAACGT AGTTTCCGCA      180
CCAGTCACCA CTGGATACAC CACTGGCTAT ACCACCGGTA ATGTCGGATA CACCACCGGA      240
GTTACTGGTT ACACCAACGG AGTTAGTGGA TATACCAATG GACTTAATGG TTATACCACT      300
GGTAGCTATG TCAGTCCCCC AGGATACACT TCTTCTGGAC TTGTCAACGT TTTCTAGATT      360
TATGATTTTCG TCTGCCCTCA ATGATGATGA CCACACTTTT TACTTTTTTAT GATATTTGGA      420
AAAAATAAAT AACTGGAAGA ATATATAATA ATTTCAAAT AAAAAAAAAA AAAAAAAAAA      480
CTCGAGGGGG                                           490

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | |
|--|-----|
| AAAAAATCGA AAGAAGGCGT AAAACCAAAA TGGGCACAGA AGGATATTCG GGATTTTAGT | 60 |
| GATGCCGACA TGGAGAGGTT ACTGGATCAA TGGGAAGAAG ATGAAGACCC CCTTCCAGAA | 120 |
| GACGAATTGC CCGAACATCT CAGACCTGAT CCAAAGATCG ACATAAGCAA CATCGATATG | 180 |
| AGCAATCCCB AAAACATACT AAAGGCTTCC AAAAAAGGCA AGACTTTGAT GGCATTTCGTA | 240 |
| CAAGTCAGTG GAAATCCAAC ACAAGAAGAA GCCGAAACCA TCACTAAATT GTGGCAAGGC | 300 |
| AGTCTATGGA ATAGTCATAT ACAAGCCGAA AGATATATGG TTAGCGATGA CAGGGCTATA | 360 |
| TTTATGTTTA AAGATGGTTC TCAAGCTTGG CCTGCTAAAG ACTTTTTAGT GGAACAAGAA | 420 |
| AGGTGTAAAG ATGTTACAAT TGAAAATAAA ATATATCCTG GTAAATATTC TTCGACTAAA | 480 |
| GAAGAATTAT AATATAATAT ATTATAATTA TAATCTATAA AATAGATTTG AAATTCTACA | 540 |
| TTCATGATCT ACTATGTATG ATATTAATTT ATTAAAAATA ATGTTTTTTC AAGTAAAAAA | 600 |
| AAAAAAAAAA AAAAAA | 616 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|--|-----|
| CTCGTGC GGG ACAGATATAG GACCGGATTC GTTAATTGAT TTGAGTGAAG TGGCTTCTGG | 60 |
| TGGTTCTGAT ATTGACACAA AATTTTCCAA TTTAAAAATA GATAAAAAGC CTGTTGCAAC | 120 |
| TTCACAACAA GGAATTGATG AATTTGATAT GTTTGCACAA TCGAGAAACA TTTCTAGTGA | 180 |
| GGGATCAACC AGTGCTATGA AGGAAGGACA CGGTTTGGAC TTATTATCAA ATACACATAA | 240 |
| AAATGTACCA CCAACAATTC CACAAGCCGG ACAACTTCCA AGGGATTCTG AGTTTGATGA | 300 |
| AATTGCTGCT TGGCTTGATG AAAAGGTTGA AGACAAAGCC CAAGTTCCCG AAGACAGTAT | 360 |
| TACAAGCAGT GAATTTGATA AATTCCTGGC AGAACGGGCA GCTGTTGCTG AAACCTTGCC | 420 |
| AAATATTCCA CCGACTACAC AAAGTAATCA TTCAAATATT GAAGCAAACG ATAAA | 475 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|---|-----|
| CCGGCACGGG AGGTAGTGAC GAAAAATAAC GATACGGGAC TCATCCGAGG CCCCCTAATC | 60 |
| GGAATGAGTA CACTTTAAAT CCTTTAACGA GGATCTATTA GAGGGCCAGT CTGTGTGCCA | 120 |
| GCAGCCGCGG TAATTCCAGC TCTAATAGCG TATATTAAAG TTGTTGCGGT TAAAAAGCTC | 180 |
| GTAGTTGAAT CTGTGTCCCA CACTGTYGGT TCACCGCTCG CGGTGTTCAA CTGGCATGTC | 240 |
| TGTGGGACGT CCTACCGGTG GGCTTAGCCC GTCAAAAGGC GGCCCAACTC AAAAT | 295 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|---|-----|
| CTGACTAATC CCAGGACTCC TTTATCCTGT TTGCGCAATG TCGATACCCA TCTACAATG | 60 |
| GTTAATGATT TATCGGCTAA ACAGAAGAGT CCTAAGAAGG TTGTTAAAGG TGTTTCTAGA | 120 |
| ATACCGACTT TTAGACCCAA GGCTATGAAT GCTGATGTTG AGAATTTTGA TTCGATGAGG | 180 |
| TGCGATGTTT GGRACAAAGA CACCAGTGTT GTTATATAAT TACTAAAGCA ATCCACATGT | 240 |
| AGCTAATTTT TTTTTTACAA TTTTATTTGT AACTATGTGT ATTTATATGA ATTCTGTGG | 300 |
| AATATAATTT TAAGTTTTTA AATGAAATAT AGATATTATT CTAAAAA AAAACAAAA | 360 |
| AAAAAAAAAA AA | 372 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|---|----|
| GGATTCGGCA CGAGAATTTA TTAAGCGCAT TATTTGCAAG TGTAATTTGC TCCTTTAACG | 60 |
|---|----|

2618-17-C4-PUS-2.txt

| | |
|--|-----|
| CGGAAGTACA AAATCGAATC GTTGGTGGCA ATGATGTAAG TATTTCAAAA ATTGGGTGGC | 120 |
| AAGTATCTAT TCAAAGTAAT AACCAACATT TCTGTGGTGG TTCAATCATT GCTAAAGATT | 180 |
| GGGTACTGAC TTCTTCTCAA TGCCTCGTGG ACAAACAAAG TCCACCGAAG GATTTAAC TG | 240 |
| TTCGTGTTGG AA | 252 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|--|-----|
| ATTCTGCTG TTAATAGTAC TAATGCAGTA ATTGCTGCHA GCTGCTGCAC AGAGGTTTTT | 60 |
| AAAATGGCAA CAAGTTGTTA CACCCACATG AACAAC TACA TGGTATTCAA TGATACCGAT | 120 |
| GGGATTTATA CATATACTTA CGAAGCTGAA AGAAAACCTG ACTGTTTAGC TTGTTACAA | 180 |
| ATTCCAAAAA CTATAGAAGT TTCTAATCCT GAAAATATGA CTCTCCAAGA CTTGATTACT | 240 |
| TTGTTGTGTG AAGGGGCTGA ATATCAAATG AAGAGCCAG GTATTGTAGC CTCAATCGAA | 300 |
| GGCAAAAACA AAACCTTATA CATGTCAACA GTAGCAAGTA TAGAAGAAAA GACTAAACAG | 360 |
| AATCTAACAA AGTCTCTAAA AGAATTAAAT CTAGAAAATG GAATGGAAC GATGGTTGCA | 420 |
| GATGTGACGA CACCAAACAC AATATTACTT AAATTAAAAT ATAAGAATGT AATTGAAAAC | 480 |
| GATGTTGAGA TGACTTGATA TTTACTTAAA AATGTTATCT TACAATAATT GATAATTTAT | 540 |
| ATTTAATACT TTTGGAACCTT TGTATTTAAT GATAATAAAT TATTATAAGA ATTAAAAAAA | 600 |
| AAAAAAAAAA AAA | 613 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|---|-----|
| TT GAT ATT TGC TCT GTT GAG GGT GCC TTA GGA TTT TTA GTG GAA ATG | 47 |
| Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met | |
| 1 5 10 15 | |
| TTA AAA TAT AAG GCC CCA AGT AAA ACT CTA GCT ATT GTA GAG AAT GCT | 95 |
| Leu Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala | |
| 20 25 30 | |
| GGT GGA ATA TTA CGA AAT GTA TCT AGT CAT ATA GCC CTT AGA GAG GAC | 143 |
| Gly Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp | |
| 35 40 45 | |
| TAC AGA GAA ATA CTT CGA CAT CAT AAT TGC TTA ACA ATA TTA CTA CAA | 191 |
| Tyr Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln | |
| 50 55 60 | |
| CAA TTA AAA TCA CCA AGC CTC ATA ATT GTC AGT AAT GCT TGT GGG ACA | 239 |
| Gln Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr | |
| 65 70 75 | |
| TTA TGG AAT TTA TCT GCT AGG AAT TCA ACA GAT CAA CAA TTT TTA TGG | 287 |
| Leu Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp | |
| 80 85 90 95 | |
| GAG AAT GGT GCT GTC CCT TTA TTA AGA AGT TTG ATA TAT TCT AAG CAT | 335 |
| Glu Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His | |
| 100 105 110 | |
| AAA ATG ATA TCT ATG GGA TCA AGT GCA GCT CTC AAA AAT TTG TTA AAT | 383 |
| Lys Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn | |
| 115 120 125 | |
| GCA AAA CCT GAG TGC ATC AAT TTC TTA AGT GAT TCT TCT TCT AAA GGA | 431 |
| Ala Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly | |
| 130 135 140 | |
| GTT CCA AAT CTA ACT ACA TTG GGT GTA AGA AAA CAA AAA TCT CTA CAT | 479 |
| Val Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His | |
| 145 150 155 | |
| GAG TTA ATA GAT CAA AAT CTT TCA GAA ACT TGT GAT AAT ATA GAT AGT | 527 |
| Glu Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser | |
| 160 165 170 175 | |
| GTG GCC GCT AA | 538 |
| Val Ala Ala | |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met Leu
 1 5 10 15
 Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala Gly
 20 25 30
 Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp Tyr
 35 40 45
 Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln Gln
 50 55 60
 Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr Leu
 65 70 75 80
 Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp Glu
 85 90 95
 Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His Lys
 100 105 110
 Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn Ala
 115 120 125
 Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly Val
 130 135 140
 Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His Glu
 145 150 155 160
 Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser Val
 165 170 175
 Ala Ala

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CTT CTT AAA CAG TTG GAC TCT GGA TTG TTA CTT GTT ACA GGT CCC 48
 Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
 1 5 10 15
 TTC TTA ATC AAT GCA TGC CCA TTG CGT CGC ATT TCC CAA AAC TAT GTC 96

2618-17-C4-PUS-2.txt

```

Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
      20              25              30
ATT GCC ACC TCT ACC CGA TTA GAC GTT AGT GGA GTT AAA TTA CCA GAA      144
Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
      35              40              45
CAC ATC AAT GAT GAT TAT TTC AAA AGG CAA AAG AAC AAG CGT GCA AAG      192
His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
      50              55              60
AAA GAG GAA GGT GAT ATT TTT GCT GCC AAG AAA GAG GCT TAT AAA CCA      240
Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
      65              70              75              80
ACT GAG CAA AGG AAG AAT GAC CAA AAG CTT GTA GAC AAA ATG GTT TTA      288
Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu
      85              90              95
GGA GTA ATC AAG AAG CAC CCA GAC CAC AAA CTT TTG TAT ACA TAT TTG      336
Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu
      100              105              110
TCA GCT ATG TTT GGT TTG AAA TCT TCC CAA TAT CCA CAT CGT ATG AAG      384
Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
      115              120              125
TTC T AAATACTATA TTCATAAAAT AAATTGAACT TCTCAAAAAA AAAA      432
Phe

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
  1              5              10              15
Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
      20              25              30
Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
      35              40              45
His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
      50              55              60
Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
      65              70              75              80
Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu

```


| | |
|---|-----|
| CCTAACATGT TTTGCCTCCA ATTTATTTTA ACAGCAAATT GCTGGGAACT TACCGTACCG | 465 |
| TAACAAAATG TTCAAGAAAT ACTGAATGTT TACAAATAGA TTATTATAAA TATTGTAACA | 525 |
| TTGTCTAATA TTTATAAGAA TTATATAAAC TGAATTGCAA AAGTTGAAAA AAAAAAAAAA | 585 |
| AAAAAAAAAA | 595 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Phe | Leu | Leu | Ala | Ile | Cys | Val | Leu | Cys | Val | Leu | Leu | Asn | Gln | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Ser | Met | Ser | Lys | Met | Val | Thr | Glu | Lys | Cys | Lys | Ser | Gly | Gly | Asn | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Asn | Pro | Ser | Thr | Lys | Glu | Val | Ser | Ile | Pro | Ser | Gly | Lys | Leu | Thr | Ile | |
| | | 35 | | | | | 40 | | | | 45 | | | | | |
| Glu | Asp | Phe | Cys | Ile | Gly | Asn | His | Gln | Ser | Cys | Lys | Ile | Phe | Cys | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ser | Gln | Cys | Gly | Phe | Gly | Gly | Gly | Ala | Cys | Gly | Asn | Gly | Gly | Ser | Thr | |
| | 65 | | | | 70 | | | | 75 | | | | | 80 | | |
| Arg | Pro | Asn | Gln | Lys | His | Cys | Tyr | Cys | | | | | | | | |
| | | | | | 85 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|---|-----|
| TTTTTTTTTT TTTTTTTTTT TTTTCAACTT TTGCAATTCA GTTTATATAA TTCTTATAAA | 60 |
| TATTAGACAA TGTTACAATA TTTATAATAA TCTATTTGTA AACATTCAGT ATTTCTTGAA | 120 |
| CATTTTGTGA CGGTACGGTA AGTTCCCAGC AATTTGCTGT TAAAATAAAT TGGAGGCAAA | 180 |

| | |
|---|-----|
| ACATGTTAGG ATCATTGAAA ACTTCAAAAT TTTATGATTG CTATCTAGCA TAATTTTAGT | 240 |
| AATTTATATC AATTTGGTCT TTCATCCGGA ATATGGTTAT TCGCAATAAC AGTGTTTTTG | 300 |
| ATTTGGTCGT GTTGAACCAC CGTTTCCACA AGCACCACCT CCAAATCCAC ATTGACTTTT | 360 |
| GCAAAATATT TTGCAACTTT GATGATTTCC AATACAAAAA TCTTCAATAG TAAGCTTCCC | 420 |
| AGATGGTATT GACACCTCTT TTGTACTTGG ATTATTTCTT CCCGATTTAC ACTTTTCAGT | 480 |
| GACCATTTTT GACATAGATA CTTGATTTAA TAAAACACAC AACACGCAAA TTGCCAGTAA | 540 |
| AAATTTTCATA TCGAATTTGA AAAATTTAAT GTTAAAACAA AATATTGAAT TTCCA | 595 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | |
|---|-----|
| ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA | 48 |
| Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln | |
| 1 5 10 15 | |
| GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT | 96 |
| Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn | |
| 20 25 30 | |
| AAT CCA AGT ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT | 144 |
| Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile | |
| 35 40 45 | |
| GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA | 192 |
| Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys | |
| 50 55 60 | |
| AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA | 240 |
| Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr | |
| 65 70 75 80 | |
| CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA | 270 |
| Arg Pro Asn Gln Lys His Cys Tyr Cys Glu | |
| 85 90 | |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
 1             5             10             15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
                20             25             30
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
                35             40             45
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys
                50             55             60
Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
        65             70             75             80
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
                85             90

```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

TCGCAATAA CAGTGTTTTT GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC      60
TCCAAATCCA CATTGACTTT TGCAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA      120
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC      180
TCCCGATTTA CACTTTTCAG TGACCATTTT TGACATAGAT ACTTGATTTA ATAAAACACA      240
CAACACGCAA ATTGCCAGTA AAAATTTTCAT                                     270

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT | 48 |
| Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser | |
| 1 5 10 15 | |
| ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT | 96 |
| Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe | |
| 20 25 30 | |
| TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT | 144 |
| Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys | |
| 35 40 45 | |
| GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT | 192 |
| Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn | |
| 50 55 60 | |
| CAA AAA CAC TGT TAT TGC GAA | 213 |
| Gln Lys His Cys Tyr Cys Glu | |
| 65 70 | |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|--|
| Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser | |
| 1 5 10 15 | |
| Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe | |
| 20 25 30 | |
| Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys | |
| 35 40 45 | |
| Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn | |
| 50 55 60 | |
| Gln Lys His Cys Tyr Cys Glu | |
| 65 70 | |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

TCGCAATAA CAGTGTTCCTT GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC      60
TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA      120
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC      180
TCCCATTGTA CACTTTTCAG TGACCATTTT TGA                                     213

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

TGG AAA GTT AAT AAA AAA TGT ACA TCA GGT GGA AAA AAT CAA GAT AGA      48
Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
  1             5             10             15

AAA CTC GAT CAA ATA ATT CAA AAA GGC CAA CAA GTT AAA ATC CAA AAT      96
Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
      20             25             30

ATT TGC AAA TTA ATA CGA GAT AAA CCA CAT ACA AAT CAA GAG AAA GAA      144
Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
      35             40             45

AAA TGT ATG AAA TTT TGC AAA AAA GTT TGC AAA GGT TAT AGA GGA GCT      192
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
      50             55             60

TGT GAT GGC AAT ATT TGC TAC TGC AGC AGG CCA AGT AAT TTA GGT CCT      240
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
      65             70             75             80

GAT TGG AAA GTA AGC AAA GAA TGC AAA GAT CCC AAT AAC AAA GAT TCT      288
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
      85             90             95

```

```

CGT CCT ACG GAA ATA GTT CCA TAT CGA CAA CAA TTA GCA AAT CCA AAT      336
Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn
      100                      105                      110

ATT TGC AAA CTA AAA AAT TCA GAG ACC AAT GAA GAT TCC AAA TGC AAA      384
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
      115                      120                      125

AAA CAT TGC AAA GAA AAA TGT CGT GGT GGA AAT GAT GCT GGA TGT GAT      432
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
      130                      135                      140

GGA AAC TTT TGT TAT TGT CGA CCA AAA AAT AAA TAATAATTAT AATAAATAAA      485
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
      145                      150                      155

TTGTTATAGT TATTAGTTAT CCCATCACAT ATTAGAAAAG TGGCTTATAA TTTATGAACA      545

ATATAACACA TAAATTAGTT GTGTAATTTT GAATGTTTTT TTCAAATATA AGGCGTTTTT      605

CTAGAATATC TTGATATTAG AAACATACTT AGATTATTTT GTTGTGTATA AAATATTCAA      665

ATACGTAAGT TATATTGAAC AAAGCATTTA GAAGCTACAT TAGATATACT AAATAAGTGC      725

AAAATTGCAT GGAAACCCTT ACTGGATTTA CTACATATTT TCTTCCTAAA TATTGTCTTG      785

GTATTACTCT TATTATATAA AAATTAATAT AAAATTGTAG ACAGAGACGA ATTGGGGTAT      845

TGTTATATAT AAAAAAGTAG TGGATTATTT AATTCTAAAA AAGTTTGCAA AATGTTTCAT      905

ACATAATAAC CGAATATTTT CAAATATATA AATATTGTAA TGAATAAATG CGCATCTGTA      965

TGCTTAATAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                        1007

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
  1                      5                      10                      15

Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
      20                      25                      30

Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
      35                      40                      45

Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
      50                      55                      60

```

2618-17-C4-PUS-2.txt

Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro
65 70 75 80
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser
85 90 95
Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn
100 105 110
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys
115 120 125
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp
130 135 140
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | |
|---|-----|
| TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTATATTAAG CATACAGATG CGCATTATT | 60 |
| CATTACAATA TTTATATATT TGAAAATATT CGGTTATTAT GTATGAAACA TTTTGCAAAC | 120 |
| TTTTTTAGAA TTAAATAATC CACTACTTTT TTATATATAA CAATACCCCA ATTCGTCTCT | 180 |
| GTCTACAATT TTATATTAAT TTTTATATAA TAAGAGTAAT ACCAAGACAA TATTTAGGAA | 240 |
| GAAAATATGT AGTAAATCCA GTAAGGGTTT CCATGCAATT TTGCACTTAT TTAGTATATC | 300 |
| TAATGTAGCT TCTAAATGCT TTGTTCAATA TAACTTACGT ATTTGAATAT TTTATACACA | 360 |
| ACAAAATAAT CTAAGTTAGT TTCTAATATC AAGATATTCT AGAAAAACGC CTTATATTTG | 420 |
| AAAAAAACAT TCGAAATTAC ACAACTAATT TATGTGTTAT ATTGTTTATA AATTATAAGC | 480 |
| CACTTTTCTA ATATGTGATG GGATAACTAA TAACTATAAC AATTTATTTA TTATAATTAT | 540 |
| TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCCATCAC ATCCAGCATC ATTTCCACCA | 600 |
| CGACATTTTT CTTTGCAATG TTTTTTGCAT TTGGAATCTT CATTGGTCTC TGAATTTTTT | 660 |
| AGTTTGCAAA TATTTGGAAT TGCTAATTGT TGTCGATATG GAACTATTTT CGTAGGACGA | 720 |
| GAATCTTTGT TATTGGGATC TTTGCATTCT TTGCTTACTT TCCAATCAGG ACCTAAATTA | 780 |

```

CTTGGCCTGC TGCAGTAGCA AATATTGCCA TCACAAGCTC CTCTATAACC TTTGCAAAC 840
TTTTTGCAAA ATTTCATACA TTTTCTTTC TCTTGATTG TATGTGGTTT ATCTCGTATT 900
AATTTGCAAA TATTTTGGAT TTTAACTTGT TGGCCTTTTT GAATTATTTG ATCGAGTTTT 960
CTATCTTGAT TTTTCCACC TGATGTACAT TTTTATTAA CTTTCCA 1007

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GCA GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA 48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr
1 5 10 15

CCT TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT 96
Pro Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp
20 25 30

TCA AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC 144
Ser Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly
35 40 45

AAA TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG 192
Lys Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp
50 55 60

GAT TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT 240
Asp Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser
65 70 75

CAA GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG 288
Gln Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys
80 85 90 95

GCA GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT 336
Ala Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe
100 105 110

GGT GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA 384
Gly Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile
115 120 125

GCA CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA 432
Ala Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys

```

| 130 | 135 | 140 | |
|---|-----|-----|------|
| GAT TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT | | | 480 |
| Asp Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp | | | |
| 145 | 150 | 155 | |
| GCG ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT | | | 528 |
| Ala Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn | | | |
| 160 | 165 | 170 | 175 |
| TTA CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC | | | 576 |
| Leu Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn | | | |
| | 180 | 185 | 190 |
| AAA GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT | | | 624 |
| Lys Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr | | | |
| | 195 | 200 | 205 |
| TCT AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT | | | 672 |
| Ser Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp | | | |
| | 210 | 215 | 220 |
| ATA TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT | | | 720 |
| Ile Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly | | | |
| | 225 | 230 | 235 |
| GCT CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA | | | 768 |
| Ala Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln | | | |
| | 240 | 245 | 250 |
| GCT ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA | | | 816 |
| Ala Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys | | | |
| | 260 | 265 | 270 |
| ATT GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA | | | 864 |
| Ile Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly | | | |
| | 275 | 280 | 285 |
| GCA CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA | | | 912 |
| Ala Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile | | | |
| | 290 | 295 | 300 |
| AAA GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA | | | 960 |
| Lys Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys | | | |
| | 305 | 310 | 315 |
| CTT GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG | | | 1008 |
| Leu Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met | | | |
| | 320 | 325 | 330 |
| CTA CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA | | | 1056 |
| Leu Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys | | | |
| | 340 | 345 | 350 |
| ACG TCG TAAAAATTAA AAATAAAAAC TTTTCAATAT ATTTTCCGCT AAAATAAATA | | | 1112 |
| Thr Ser | | | |
| | | | |
| AATATGTTTG TATATTTAAA CTTATCAAAA TAATAGTAGT GTTTTAATAA AGATTTTAAA | | | |
| 1172 | | | |

TAAATAATTG TAAAAAAAAA AAAAAAAAAA AAA

1205

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
 1 5 10 15
 Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
 20 25 30
 Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
 35 40 45
 Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
 50 55 60
 Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
 65 70 75 80
 Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
 85 90 95
 Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
 100 105 110
 Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
 115 120 125
 Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
 130 135 140
 Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
 145 150 155 160
 Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
 165 170 175
 Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
 180 185 190
 Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
 195 200 205
 Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
 210 215 220
 Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala

225 230 235 240
 Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
 245 250 255
 Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
 260 265 270
 Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
 275 280 285
 Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
 290 295 300
 Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
 305 310 315 320
 Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
 325 330 335
 Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
 340 345 350
 Ser

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TTTTTTTTTT TTTTTTTTTT TTACAATTAT TTATTTAAAA TCTTTATTAA AACACTACTA 60
 TTATTTTGAT AAGTTTAAAT ATACAAACAT ATTTATTTAT TTTAGCGGAA AATATATTGA 120
 AAAGTTTTTA TTTTAAATTT TTACGACGTT TTACATAATT TATCATGAGC TTCCTTCTCC 180
 ATGTTATATT TTTGTAGCAT TGATTTGAAA GTACCATAAG AACACTTGTC ACCGCATTGT 240
 GCAAGTTTCA TTGGTTTCAG CTTCAATTTGG TCATTGTTTC TATAGAGAAC TTTTATGCTC 300
 CAATCGCTCT TATCTTGGTG TAGTTCAATA ACGTGAAGTG CTCCTTGGCC AGGATATAAA 360
 GTAGACGGAT CAAGGTCCTT ATTTTCAATT TTTGTACCTT CGGGAGCAAA TGCTGAAACA 420
 AATGCTGCTA AGATAGCTTG AGGAACGGTC AGCACTGATA ATTTGTTTTT CTTTCTCTCT 480
 GGAGCACCCG GTTGTCCCTC TCCTTTCTTT ATGTTTTTCGA TATCGTTCAA TATATCGTTA 540
 ATCATACGAC CTCCTGACAT CTTTCTAAGA TTATCATTAG AAGTCAAGGC GGTCCATAAA 600
 TATTTCTCAG AGAATTGTTT TAGATCTTTG TTTACAGTAT TCCACCATGT TGGAGCGTTA 660

| | |
|--|------|
| TTTTGCTTGC TTTGTAAATT CAAAGTTTCA TATGCCAGCC AAACATTCTG AGGGCTTGTC | 720 |
| GTCGCATCTA TTTTATACGC TTCTTTTAAT TTTGCAAGTG AATTTTTATA ATCTTTTGCA | 780 |
| CTTTTTGTGA ACAAGTCTCT TACTGCTATT TTCTGTTGTG CTATGAAGTT TGGACAAGTT | 840 |
| TTTGGAATAT AAAATTTAGC ATATTCACCA AACGAAGAAA ATATGGTTTT ATCTCCTTTC | 900 |
| TCTTTTGTCC AAAGTGCCTT TTCCTTTTCT TCTAGACCAG AACCAATGAT AAGCGCTCCT | 960 |
| TCTTGAGATC TTCTCGTAGC ACTAGCTAAT GTCCAATAAT TTTTATTTGA ATCCCATTG | 1020 |
| TCAACTTTTA AATTAGTTCT GTAATGTTTCG GATAATAATT TGCCAATTTT TAATGCCTCT | 1080 |
| TCTTGACCTG CCGGTGTCAA TTGGCTTGAA TCTTCAGACT TGTGTGTAAT TTTTGGACCG | 1140 |
| CCTGGATAAT CACAAGGTGT ATGTGACATA CCTCGTGCAG TCGCAAACAC AAATTTCAAT | 1200 |
| TCTGC | 1205 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|---|-----|
| GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA CCT | 48 |
| Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro | |
| 1 5 10 15 | |
| TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT TCA | 96 |
| Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser | |
| 20 25 30 | |
| AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC AAA | 144 |
| Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys | |
| 35 40 45 | |
| TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG GAT | 192 |
| Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp | |
| 50 55 60 | |
| TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT CAA | 240 |
| Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln | |
| 65 70 75 80 | |
| GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG GCA | 288 |

2618-17-C4-PUS-2.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Gly | Ala | Leu | Ile | Ile | Gly | Ser | Gly | Leu | Glu | Glu | Lys | Glu | Lys | Ala | | |
| | | | | 85 | | | | | 90 | | | | | | 95 | | |
| GTT | TGG | ACA | AAA | GAG | AAA | GGA | GAT | AAA | ACC | ATA | TTT | TCT | TCG | TTT | GGT | 336 | |
| Val | Trp | Thr | Lys | Glu | Lys | Gly | Asp | Lys | Thr | Ile | Phe | Ser | Ser | Phe | Gly | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| GAA | TAT | GCT | AAA | TTT | TAT | AGT | CCA | AAA | ACT | TGT | CCA | AAC | TTC | ATA | GCA | 384 | |
| Glu | Tyr | Ala | Lys | Phe | Tyr | Ser | Pro | Lys | Thr | Cys | Pro | Asn | Phe | Ile | Ala | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | |
| CAA | CAG | AAA | ATA | GCA | GTA | AGA | GAC | TTG | TTA | ACA | AAA | AGT | GCA | AAA | GAT | 432 | |
| Gln | Gln | Lys | Ile | Ala | Val | Arg | Asp | Leu | Leu | Thr | Lys | Ser | Ala | Lys | Asp | | |
| | | | 130 | | | 135 | | | | | | 140 | | | | | |
| TAT | AAA | AAT | TCA | CTT | GCA | AAA | TTA | AAA | GAA | GCG | TAT | AAA | ATA | GAT | GCG | 480 | |
| Tyr | Lys | Asn | Ser | Leu | Ala | Lys | Leu | Lys | Glu | Ala | Tyr | Lys | Ile | Asp | Ala | | |
| | | | | | 150 | | | | | 155 | | | | | 160 | | |
| ACG | ACA | AGC | CCT | CAG | AAT | GTT | TGG | CTG | GCA | TAT | GAA | ACT | TTG | AAT | TTA | 528 | |
| Thr | Thr | Ser | Pro | Gln | Asn | Val | Trp | Leu | Ala | Tyr | Glu | Thr | Leu | Asn | Leu | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| CAA | AGC | AAG | CAA | AAT | AAC | GCT | CCA | ACA | TGG | TGG | AAT | ACT | GTA | AAC | AAA | 576 | |
| Gln | Ser | Lys | Gln | Asn | Asn | Ala | Pro | Thr | Trp | Trp | Asn | Thr | Val | Asn | Lys | | |
| | | | 180 | | | | 185 | | | | | | 190 | | | | |
| GAT | CTA | AAA | CAA | TTC | TCT | GAG | AAA | TAT | TTA | TGG | ACC | GCC | TTG | ACT | TCT | 624 | |
| Asp | Leu | Lys | Gln | Phe | Ser | Glu | Lys | Tyr | Leu | Trp | Thr | Ala | Leu | Thr | Ser | | |
| | | | 195 | | | | 200 | | | | | 205 | | | | | |
| AAT | GAT | AAT | CTT | AGA | AAG | ATG | TCA | GGA | GGT | CGT | ATG | ATT | AAC | GAT | ATA | 672 | |
| Asn | Asp | Asn | Leu | Arg | Lys | Met | Ser | Gly | Gly | Arg | Met | Ile | Asn | Asp | Ile | | |
| | | | 210 | | | 215 | | | | | 220 | | | | | | |
| TTG | AAC | GAT | ATC | GAA | AAC | ATA | AAG | AAA | GGA | GAG | GGA | CAA | CCG | GGT | GCT | 720 | |
| Leu | Asn | Asp | Ile | Glu | Asn | Ile | Lys | Lys | Gly | Glu | Gly | Gln | Pro | Gly | Ala | | |
| | | | | | 230 | | | | | 235 | | | | | 240 | | |
| CCA | GGA | GGA | AAG | GAA | AAC | AAA | TTA | TCA | GTG | CTG | ACC | GTT | CCT | CAA | GCT | 768 | |
| Pro | Gly | Gly | Lys | Glu | Asn | Lys | Leu | Ser | Val | Leu | Thr | Val | Pro | Gln | Ala | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| ATC | TTA | GCA | GCA | TTT | GTT | TCA | GCA | TTT | GCT | CCC | GAA | GGT | ACA | AAA | ATT | 816 | |
| Ile | Leu | Ala | Ala | Phe | Val | Ser | Ala | Phe | Ala | Pro | Glu | Gly | Thr | Lys | Ile | | |
| | | | | 260 | | | | 265 | | | | | 270 | | | | |
| GAA | AAT | AAG | GAC | CTT | GAT | CCG | TCT | ACT | TTA | TAT | CCT | GGC | CAA | GGA | GCA | 864 | |
| Glu | Asn | Lys | Asp | Leu | Asp | Pro | Ser | Thr | Leu | Tyr | Pro | Gly | Gln | Gly | Ala | | |
| | | | | 275 | | | 280 | | | | | 285 | | | | | |
| CTT | CAC | GTT | ATT | GAA | CTA | CAC | CAA | GAT | AAG | AGC | GAT | TGG | AGC | ATA | AAA | 912 | |
| Leu | His | Val | Ile | Glu | Leu | His | Gln | Asp | Lys | Ser | Asp | Trp | Ser | Ile | Lys | | |
| | | | | 290 | | | 295 | | | | 300 | | | | | | |
| GTT | CTC | TAT | AGA | AAC | AAT | GAC | CAA | ATG | AAG | CTG | AAA | CCA | ATG | AAA | CTT | 960 | |
| Val | Leu | Tyr | Arg | Asn | Asn | Asp | Gln | Met | Lys | Leu | Lys | Pro | Met | Lys | Leu | | |
| | | | | 305 | | 310 | | | | 315 | | | | | 320 | | |

2618-17-C4-PUS-2.txt

| | |
|---|------|
| GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG CTA | 1008 |
| Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu | |
| 325 330 335 | |
| | |
| CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA ACG | 1056 |
| Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr | |
| 340 345 350 | |
| | |
| TCG | 1059 |
| Ser | |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|---|--|
| Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro | |
| 1 5 10 15 | |
| Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser | |
| 20 25 30 | |
| Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys | |
| 35 40 45 | |
| Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp | |
| 50 55 60 | |
| Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln | |
| 65 70 75 80 | |
| Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala | |
| 85 90 95 | |
| Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly | |
| 100 105 110 | |
| Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala | |
| 115 120 125 | |
| Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp | |
| 130 135 140 | |
| Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala | |
| 145 150 155 160 | |
| Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu | |
| 165 170 175 | |
| Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys | |
| 180 185 190 | |

2618-17-C4-PUS-2.txt

Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
195 200 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
210 215 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225 230 235 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
245 250 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
260 265 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
290 295 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305 310 315 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
325 330 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
340 345 350

Ser

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|---|-----|
| CGACGTTTTA CATAATTTAT CATGAGCTTC CTTCTCCATG TTATATTTTT GTAGCATTGA | 60 |
| TTTGAAAGTA CCATAAGAAC ACTTGTCAAC GCATTGTGCA AGTTTCATTG GTTTCAGCTT | 120 |
| CATTTGGTCA TTGTTTCTAT AGAGAACTTT TATGCTCCAA TCGCTCTTAT CTTGGTGTAG | 180 |
| TTCAATAACG TGAAGTGCTC CTTGGCCAGG ATATAAAGTA GACGGATCAA GGTCCTTATT | 240 |
| TTCAATTTTT GTACCTTCGG GAGCAAATGC TGAAACAAAT GCTGCTAAGA TAGCTTGAGG | 300 |

```

AACGGTCAGC ACTGATAATT TGTTCCTCTT TCCTCCTGGA GCACCCGGTT GTCCCTCTCC      360
TTTCTTTATG TTTTCGATAT CGTTCAATAT ATCGTTAATC ATACGACCTC CTGACATCTT      420
TCTAAGATTA TCATTAGAAG TCAAGGCGGT CCATAAATAT TTCTCAGAGA ATTGTTTTAG      480
ATCTTTGTTT ACAGTATTCC ACCATGTTGG AGCGTTATTT TGCTTGCTTT GTAAATTCAA      540
AGTTTCATAT GCCAGCCAAA CATTCTGAGG GCTTGTCGTC GCATCTATTT TATACGCTTC      600
TTTTAATTTT GCAAGTGAAT TTTTATAATC TTTTGCACTT TTTGTTAACA AGTCTCTTAC      660
TGCTATTTTC TGTTGTGCTA TGAAGTTTGG ACAAGTTTTT GGACTATAAA ATTTAGCATA      720
TTCACCAAAC GAAGAAAATA TGGTTTTTATC TCCTTTCTCT TTTGTCCAAA CTGCCTTTTC      780
CTTTTCTTCT AGACCAGAAC CAATGATAAG CGCTCCTTCT TGAGATCTTC TCGTAGCACT      840
AGCTAATGTC CAATAATTTT TATTTGAATC CCATTTGTCA ACTTTTAAAT TAGTTCTGTA      900
ATGTTCCGAT AATAATTTGC CAATTTTTAA TGCCTCTTCT TGACCTGCCG GTGTCAATTG      960
GCTTGAATCT TCAGACTTGT GTGTAATTTT TGGACCGCCT GGATAATCAC AAGGTGTATG     1020
TGACATACCT CGTGCAGTCG CAAACACAAA TTTCAATTC                               1059

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Xaa Glu Leu Lys Phe Val Phe Val Met Val Lys Gly Pro Asp His Glu
1           5           10          15
Ala Cys Asn Tyr Ala Gly Gly Xaa Gln
          20          25

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|-----|
| ATG GTT AAA GGT CCA GAT CAC GAA GCT TGT AAC TAT GCA GGA GGT CCT | 48 |
| Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro | |
| 1 5 10 15 | |
| CAG TTA ACT ACT CTT CAA GAA AAA GAT AGT GTT CTA ACT GAA GAT GGC | 96 |
| Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly | |
| 20 25 30 | |
| AAG ACA GAA GCA TAC GAA TTG GGA AAA CTT TTG GAC AAG GTA TAT AAA | 144 |
| Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys | |
| 35 40 45 | |
| AAA CAA TTA AAA GTT GAC AAA TGG GAT GCC ACG AAA ACC TAC TGG GCT | 192 |
| Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala | |
| 50 55 60 | |
| GTG TCC ACA AAA GCT ATG CGT ACT AAA GAA GCA GCC TTA ATT GTA GGA | 240 |
| Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly | |
| 65 70 75 80 | |
| GCA GGA TTG GAA AAT AAT CCT GCA AAA GCT AAA GGT AAT TGG ACA CAA | 288 |
| Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln | |
| 85 90 95 | |
| CAA CAG CTC GAT TCA ACA CAT TTT GAT GCG ATG CCT GGC TTT TCT AGA | 336 |
| Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg | |
| 100 105 110 | |
| TTT TGG AAT CCT CAA CAA TGT CCG GCA TAT TTC AGA GCG CTC TCG CTA | 384 |
| Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu | |
| 115 120 125 | |
| CAA AAT CAG AAA ATA AAG AAA T | 406 |
| Gln Asn Gln Lys Ile Lys Lys | |
| 130 135 | |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro

1 5 10 15
 Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly
 20 25 30
 Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys
 35 40 45
 Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala
 50 55 60
 Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly
 65 70 75 80
 Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln
 85 90 95
 Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg
 100 105 110
 Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu
 115 120 125
 Gln Asn Gln Lys Ile Lys Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AATTTCTTTA TTTTCTGATT TTGTAGCGAG AGCGCTCTGA AATATGCCGG ACATTGTTGA 60
 GGATTCCAAA ATCTAGAAAA GCCAGGCATC GCATCAAAAT GTGTTGAATC GAGCTGTTGT 120
 TGTGTCCAAT TACCTTTAGC TTTTGCAGGA TTATTTTCCA ATCCTGCTCC TACAATTAAG 180
 GCTGCTTCTT TAGTACGCAT AGCTTTTGTG GACACAGCCC AGTAGGTTTT CGTGGCATCC 240
 CATTTGTCAA CTTTAAATTG TTTTATATAT ACCTTGTTCCA AAAGTTTTCC CAATTCGTAT 300
 GCTTCTGTCT TGCCATCTTC AGTTAGAACA CTATCTTTTT CTTGAAGAGT AGTTAACTGA 360
 GGACCTCCTG CATAGTTACA AGCTTCGTGA TCTGGACCTT TAACCAT 407

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | |
|---|-----|
| GAA GTT ATG GAT AAA TTG CGA AAA CAG GCA CCT CCT AAA ACT GAT GGC | 48 |
| Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly | |
| 1 5 10 15 | |
| AAT CCT CCA AAA ACA ACC ATA ATG AGT ACA CTT CAA AAG CAA CAA ATA | 96 |
| Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile | |
| 20 25 30 | |
| AGT TGC ACA GAA GTG AAA GCG GTT AAC TTA GAA AGT CAT GTT TGT GCT | 144 |
| Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala | |
| 35 40 45 | |
| TAT GAT TGT AGT CAA CCT GAA ACT GCA GGA ATT ACA TGC AAA GGA AAT | 192 |
| Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn | |
| 50 55 60 | |
| AAG TGT GAT TGT CCT AAA AAA CGC TAAAAATTTA TTCAAAACAT TTACATTTTT | 246 |
| Lys Cys Asp Cys Pro Lys Lys Arg | |
| 65 70 | |
| TATTAATATT CAACTATCAA AAATTCTGTG TTGATTGTTA TTATATTTAT CATAGTTACT | 306 |
| AGAAATAAAA TTTTATAACA TTGTTAATTC GAAATTGAAT ACACATAATA TTATAATTAG | 366 |
| TGAGGTTAAA AGAAATAAAC CGAATATCCA AATCAAAAAA AAAAAAAAAA AAAA | 420 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | |
|---|--|
| Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly | |
| 1 5 10 15 | |
| Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile | |
| 20 25 30 | |
| Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala | |
| 35 40 45 | |

Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn
 50 55 60

Lys Cys Asp Cys Pro Lys Lys Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

TTTTTTTTTT TTTTTTTTTT GATTGGATA TTCGGTTTAT TTCTTTTAAC CTCACTAATT      60
ATAATATTAT GTGTATTCAA TTTCGAATTA ACAATGTTAT AAAATTTTAT TTCTAGTAAC      120
TATGATAAAT ATAATAACAA TCAACACAGA ATTTTGGATA GTTGAATATT AATAAAAAAT      180
GTAAATGTTT TGAATAAATT TTTAGCGTTT TTTAGGACAA TCACACTTAT TTCCTTTGCA      240
TGTAATTCCT GCAGTTTCAG GTTGACTACA ATCATAAGCA CAAACATGAC TTTCTAAGTT      300
AACCGCTTTC ACTTCTGTGC AACTTATTTG TTGCTTTTGA AGTGTACTCA TTATGGTTGT      360
TTTTGGAGGA TTGCCATCAG TTTTAGGAGG TGCCTGTTTT CGCAATTTAT CCATAACTTC      420

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
1           5           10           15
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
          20           25           30
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
          35           40           45
Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn
50           55           60

```


2618-17-C4-PUS-2.txt
 Gln Lys His Cys Tyr Cys Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Lys | Leu | Gln | Phe | Val | Phe | Val | Met | Ala | Arg | Gly | Pro | Asp | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Glu | Ala | Cys | Asn | Tyr | Pro | Gly | Gly | Pro | | | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGTGGATCCG TCAAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCGGAATTCG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGCGGATCC GCATATGGAA GACATCTGGA AAGTTAATAA AAAATGTACA TCAG

54

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCGGAATTCT TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCC

45

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAATTTGTAT TTTGTATATG GTATAAAGGA TCCATGATCA TGAAGC

46

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..37
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGAACCAT GGATAATACA TCGATAAAGA TACTACG

37

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:

2618-17-C4-PUS-2.txt

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAAGTATATG GACTAAATTA GAGAGCAAGG C

31

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Phe | Asn | Lys | Leu | Val | Gln | Ser | Trp | Thr | Glu | Pro | Met | Val | Phe | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Tyr Pro Tyr

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTAATACGAC TCACTATATA GGGC